

SEQUENCE LISTING

<110> Aharoni, Asaph
Lucker, Joost
Verhoeven, Harrie A.
van Tunen, Arjen J.
O'Connell, Ann P.

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<150> EP 98204018.0

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140	145	150	155	
att ggg ttg ccg gac ttc agt caa gag ctc cgg tgc ttt cag acc gtg	590			
Ile Gly Leu Pro Asp Phe Ser Gln Glu Leu Arg Cys Phe Gln Thr Val				
160	165	170		
act tgc ttt cag gct gtg gtg aat aat ctg gag gat gca cat gag atg	638			
Thr Cys Phe Gln Ala Val Val Asn Asn Leu Glu Asp Ala His Glu Met				
175	180	185		
att gat act gca att tcg act gcg ttg aaa gaa agc aag cct gtg tat	686			
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atc agc att ggc tgc aac ttg gct ggg att cct cat cct act ttc agc	734			
Ile Ser Ile Gly Cys Asn Leu Ala Gly Ile Pro His Pro Thr Phe Ser				
205	210	215		
cgt gaa cct gtt cca ttt tca ttg tct cca aaa ttg agc aat aag tgg	782			
Arg Glu Pro Val Pro Phe Ser Leu Ser Pro Lys Leu Ser Asn Lys Trp				
220	225	230	235	
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Gly Leu Glu Ala Ala Val Glu Ala Ala Ala Glu Phe Leu Asn Lys Ala				
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Gly Asp Ala Phe Val Glu Leu Ala Asp Ala Ser Gly Phe Ala Leu Ala				
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Val Met Pro Ser Ala Lys Gly Gln Val Pro Glu His His Pro His Phe				
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Val Glu Ser Ala Asp Ala Tyr Leu Phe Ala Gly Pro Ile Phe Asn Asp				
320	325	330		
tac agc tca gtt ggg tac tcg ctc ctt ctc aag aaa gag aag gcg atc	1118			
Tyr Ser Ser Val Gly Tyr Ser Leu Leu Leu Lys Lys Glu Lys Ala Ile				
335	340	345		
att gtg cag cca gat cgt gtg acg ata ggg aat ggc cct aca ttt ggt	1166			
Ile Val Gln Pro Asp Arg Val Thr Ile Gly Asn Gly Pro Thr Phe Gly				
350	355	360		
tgt gtt ctc atg aag gat ttc ctc tta ggc cta gca aag aag ctg aag	1214			
Cys Val Leu Met Lys Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys				
365	370	375		
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His Asn Asn Thr Ala His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp				
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Gly His Pro Leu Lys Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val	
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Leu Phe Lys His Ile Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile	
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Pro Gly Cys Gly Tyr Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp	
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Ser Val Gly Ala Thr Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg	
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Val Ile Ser Phe Ile Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp	
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Val Ser Thr Met Ile Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile	
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Asn Asn Gly Gly Tyr Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr	
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Asn Val Ile Lys Asn Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His	
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Asn Gly Glu Gly Lys Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu	
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Leu Ile Glu Ala Ile Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe	
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Cys Phe Ile Glu Val Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu	
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Leu Glu Trp Gly Ser Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn	
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2141

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11

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gtt aca gtg att agt aca tcc cct aag aaa gag gag gaa gct cgt aaa Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Arg Lys 210 215 220 225			730
cac cta gga gct gac tcg ttt ttg gtt agc cgt gac caa gat caa atg His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met 230 235 240			778
cag gct gcc att ggt acc atg gat ggg atc att gac acg gtt tct gca Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala 245 250 255			826
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ctt gtt atg gtt ggt gca cca gag aag cct ctt gaa ctg cca gtt ttt Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe 275 280 285			922
cct tta ctc atg gga aga aag atg gta gct ggt agc ggc att ggg ggt Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly Gly 290 295 300 305			970
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aca gca gac atc gaa gtc ata cca atc gac tac ttg taacactgct Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu 325 330			1064
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Gln Leu Thr Pro Pro Ala Tyr Val Pro Ile Val Phe Phe Tyr Pro Ile	35	40	45
Thr Asp His Asp Phe Asn Leu Pro Gln Thr Leu Ala Asp Leu Arg Gln	50	55	60
Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val	65	70	75
Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu	85	90	95
Glu Ala Arg Val Asn Cys Asp Met Thr Asp Phe Leu Arg Leu Arg Lys	100	105	110
Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu	115	120	125
Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Val	130	135	140
Phe Asp Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile	145	150	155
Asp Gly Gly Thr Ala Asp Cys Phe Leu Lys Ser Trp Gly Ala Val Phe	165	170	175
Arg Gly Cys Arg Glu Asn Ile Ile His Pro Ser Leu Ser Glu Ala Ala	180	185	190
Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Val Asp Gln	195	200	205
Met Glu Ala Leu Trp Phe Ala Gly Lys Lys Val Ala Thr Arg Arg Phe	210	215	220
Val Phe Gly Val Lys Ala Ile Ser Ser Ile Gln Asp Glu Ala Lys Ser	225	230	235
Glu Ser Val Pro Lys Pro Ser Arg Val His Ala Val Thr Gly Phe Leu	245	250	255
Trp Lys His Leu Ile Ala Ala Ser Arg Ala Leu Thr Ser Gly Thr Thr	260	265	270
Ser Thr Arg Leu Ser Ile Ala Ala Gln Ala Val Asn Leu Arg Thr Arg	275	280	285
Met Asn Met Glu Thr Val Leu Asp Asn Ala Thr Gly Asn Leu Phe Trp	290	295	300
Trp Ala Gln Ala Ile Leu Glu Leu Ser His Thr Thr Pro Glu Ile Ser	305	310	315
Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys	325	330	335

Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Lys Gly Lys Glu Gly Tyr
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 Gly Arg Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
 355 360 365
 Glu Pro Ala Pro Asp Ile Tyr Leu Phe Ser Ser Trp Thr Asn Phe Phe
 370 375 380
 Asn Pro Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
 385 390 395 400
 Gly Lys Ile Glu Ser Ala Ser Cys Lys Phe Ile Ile Leu Val Pro Thr
 405 410 415
 Gln Cys Gly Ser Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
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 gga ggt gtt gga cac atg ggg gtg aag ata gca aag gct atg gga cac 95
 Gly Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His
 20 25 30
 cat atc acc gtg ata agc tct tct gat aag aag aaa aaa gag gcc ttg 143
 His Ile Thr Val Ile Ser Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu
 35 40 45
 gag cat att ggt gct gat gag tac ttg gtg agc tct gat gcc acc caa 191
 Glu His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln
 50 55 60
 atg caa gag gct atg gac tca ctg gat tac att att gac acc att cca 239
 Met Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro
 65 70 75
 gtg ttc cac cct ctt gag cct tac ctc tct ttg ttg aag ctt gat ggg 287
 Val Phe His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly

80	85	90	95	
aag ttg atc ttg atg ggt gtt atc aac acc cca ttg caa ttt gtc tct				335
Lys Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser	100	105	110	
cca ttg gtc atg ctt ggg gag gaa gac gat cac cgg gag ctt tgt ggg				383
Pro Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly	115	120	125	
gag cat gaa gga gat gga gga gat gct cga gtt ctg caa aga gaa aga				431
Glu His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg	130	135	140	
gct gaa acg atg att gaa gtg gtg aag atg gac tac atc aac gaa gct				479
Ala Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala	145	150	155	
ttc gaa agg ttg gag aag aac gac gtt agg tac agg ttc gtt gtg gat				527
Phe Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp	160	165	170	175
tgt tgc cgg cag caa tct tgatcaataa gaaagaaaga aggcattcatc				575
Cys Cys Arg Gln Gln Ser	180			
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tgt gaa gac gag ttt aaa aag ata atg aag ata aat ttc atg tct gca				96
Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala	20	25	30	
tgg ttt ctg gta aat gcc gtt ggc aga aga atg cga gat cat aaa tca				144
Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser	35	40	45	
gga ggt tcc atc ata ttg ttg acc tcg att gtt gga gct gaa aga ggg				192
Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly	50	55	60	
ctt tat aca gga gct gtt gcc tat ggt gca tgt tcg gca gca ctg cag				240
Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln				

65	70	75	80	
cag tta gta agg tcg tcg gca ttg gag att gga aaa tac cag atc agg				288
Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg	85	90	95	
gtt aat gca atc gca cgt ggt ttg cat ttg gaa gat gag ttt cct aag				336
Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys	100	105	110	
tct gtg gga ata gag aga gca aag aag ctg gtg aat gat gca gtt ccg				384
Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro	115	120	125	
ctg gag aga tgg ctt gat gtt aaa aat gat gtg gct tca agt gtc ata				432
Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile	130	135	140	
tat ttg gtc agt gat ggt tca agg tac atg acg ggc aca act ata ttt				480
Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe	145	150	155	160
gtt gat ggg gca cag tct ctc gtg agg cct cga atg cgt tct tat atg				528
Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met	165	170	175	
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Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro	1	5	10	
gag att gcg agg agg agg aat gcg cac ttg cag aag cac cct gat gcg				158
Glu Ile Ala Arg Arg Arg Asn Ala His Leu Gln Lys His Pro Asp Ala	15	20	25	
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Lys Ile Ile Pro Leu Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu	30	35	40	
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Tyr Ile Thr Ser Ala Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu				

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320 325 330

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335 340 345

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365 370 375

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Tyr Lys

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Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp
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	50					55					60					
gca	att	gga	aag	gcg	ttg	gtg	ttc	tac	tat	cct	tta	gca	gga	aga	ttg	240
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aga	gaa	ggg	cca	ggg	aga	aag	ctt	ttt	gtt	gaa	tgt	aca	ggg	gaa	gga	288
Arg	Glu	Gly	Pro	Gly	Arg	Lys	Leu	Phe	Val	Glu	Cys	Thr	Gly	Glu	Gly	
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Ile	Leu	Phe	Ile	Glu	Ala	Asp	Ala	Asp	Val	Ser	Leu	Glu	Glu	Phe	Trp	
			100					105					110			
gat	act	ctt	cca	tat	tca	ctt	tca	agc	atg	cag	aac	aat	att	ata	cat	384
Asp	Thr	Leu	Pro	Tyr	Ser	Leu	Ser	Ser	Met	Gln	Asn	Asn	Ile	Ile	His	
		115					120					125				
aac	gct	tta	aat	tct	gat	gaa	gtc	ctc	aat	tct	cca	tta	ttg	ctc	att	432
Asn	Ala	Leu	Asn	Ser	Asp	Glu	Val	Leu	Asn	Ser	Pro	Leu	Leu	Leu	Ile	
	130					135					140					
cag	gtg	aca	cga	ctc	aag	tgt	gga	ggg	ttc	att	ttt	ggg	ctt	tgt	ttc	480
Gln	Val	Thr	Arg	Leu	Lys	Cys	Gly	Gly	Phe	Ile	Phe	Gly	Leu	Cys	Phe	
	145				150					155					160	
aat	cat	act	atg	gca	gat	ggg	ttt	ggg	att	gtc	caa	ttc	atg	aag	gct	528
Asn	His	Thr	Met	Ala	Asp	Gly	Phe	Gly	Ile	Val	Gln	Phe	Met	Lys	Ala	
				165					170					175		
aca	gcg	gag	ata	gct	cgt	gga	gct	ttt	gct	cca	tct	att	tta	cca	gta	576
Thr	Ala	Glu	Ile	Ala	Arg	Gly	Ala	Phe	Ala	Pro	Ser	Ile	Leu	Pro	Val	
			180				185						190			
tgg	caa	aga	gct	ctc	tta	acc	gca	aga	gac	cct	ccc	aga	atc	act	ttt	624
Trp	Gln	Arg	Ala	Leu	Leu	Thr	Ala	Arg	Asp	Pro	Pro	Arg	Ile	Thr	Phe	
		195					200					205				
cgc	cac	tat	gaa	tac	gac	caa	gta	gtc	gac	atg	aag	agc	ggc	ctc	att	672
Arg	His	Tyr	Glu	Tyr	Asp	Gln	Val	Val	Asp	Met	Lys	Ser	Gly	Leu	Ile	
	210					215					220					
cca	gtc	aat	agc	aag	atc	gat	caa	tta	ttc	ttc	ttt	agc	caa	ctt	caa	720
Pro	Val	Asn	Ser	Lys	Ile	Asp	Gln	Leu	Phe	Phe	Phe	Ser	Gln	Leu	Gln	
	225				230				235					240		
atc	tcc	acc	ctt	cgc	caa	act	ttg	cca	gcc	cac	ctt	cac	gat	tgc	cct	768
Ile	Ser	Thr	Leu	Arg	Gln	Thr	Leu	Pro	Ala	His	Leu	His	Asp	Cys	Pro	
				245					250					255		
tcc	ttc	gag	gtc	ctc	act	gcc	tat	gtt	tgg	cgc	ctc	cgt	acc	ata	gcc	816
Ser	Phe	Glu	Val	Leu	Thr	Ala	Tyr	Val	Trp	Arg	Leu	Arg	Thr	Ile	Ala	
			260					265					270			
ctt	caa	ttt	aag	cca	gag	gag	gaa	gtg	cgg	ttt	ctt	tgc	gta	atg	aat	864
Leu	Gln	Phe	Lys	Pro	Glu	Glu	Glu	Val	Arg	Phe	Leu	Cys	Val	Met	Asn	
		275					280					285				
cta	cgc	tcg	aag	atc	gac	ata	cca	tta	ggg	tat	tat	ggg	aat	gcg	gta	912
Leu	Arg	Ser	Lys	Ile	Asp	Ile	Pro	Leu	Gly	Tyr	Tyr	Gly	Asn	Ala	Val	

290	295	300	
ggt ggt cct gca gta atc acc acc gct gcg aag ctt tgt ggg aac cca			960
Val Val Pro Ala Val Ile Thr Thr Ala Ala Lys Leu Cys Gly Asn Pro			
305	310	315	320
ctt ggt tat gct gta gac ttg att agg aag gcc aag gct aag gca acg			1008
Leu Gly Tyr Ala Val Asp Leu Ile Arg Lys Ala Lys Ala Lys Ala Thr			
	325	330	335
atg gag tac ata aag tct acg gtg gat ctt atg gtg att aaa gga cga			1056
Met Glu Tyr Ile Lys Ser Thr Val Asp Leu Met Val Ile Lys Gly Arg			
	340	345	350
ccc tat ttc act gta gtt gga tca ttt atg atg tca gac cta acg aga			1104
Pro Tyr Phe Thr Val Val Gly Ser Phe Met Met Ser Asp Leu Thr Arg			
	355	360	365
att ggg gtt gaa aac gtg gac ttt gga tgg gga aag gcc att ttt gga			1152
Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly			
	370	375	380
gga cct aca acc aca ggg gcc aga att aca cga ggt ttg gta agc ttt			1200
Gly Pro Thr Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe			
	385	390	400
tgt gta cct ttc atg aat aga aat gga gaa aag gga act gcg tta agt			1248
Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser			
	405	410	415
cta tgc ttg cct cct cca gcc atg gaa aga ttt agg gca aat gtt cat			1296
Leu Cys Leu Pro Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His			
	420	425	430
gcc tcg ttg caa gtg aaa caa gtg gtt gat gca gtt gat agc cat atg			1344
Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met			
	435	440	445
caa act att caa tct gct tcg aaa taaataatat tgttgaaggt gggctctgagt			1398
Gln Thr Ile Gln Ser Ala Ser Lys			
	450	455	
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gctgagttgc tgt			1471
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Met Ser Phe Ser Val Leu Gln Val Lys Arg Leu Gln Pro Glu Leu Ile			

1	5	10	15	
act ccg gca aag tca acg cct caa gaa aca aag ttt ctc tca gat att	Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile	96		
	20 25 30			
gac gac caa gaa agc ttg aga gtt cag att cca atc ata atg tgt tac	Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr	144		
	35 40 45			
aaa gac aac cct tca ctt aat aaa aat cgt aat ccc gtt aag gca att	Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile	192		
	50 55 60			
agg gaa gcc tta agt aga gca tta gtg tat tac tac ccc tta gct gga	Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly	240		
	65 70 75 80			
agg ctt agg gaa ggg cct aat aga aag ctc gtg gtc gat tgc aat ggt	Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly	288		
	85 90 95			
gaa ggt atc ttg ttc gtt gag gct tct gct gat gtc aca ctt gag caa	Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln	336		
	100 105 110			
cta gga gac aaa att cta ccc cct tgt cca ctt tta gag gag ttc tta	Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu	384		
	115 120 125			
tat aat ttt cca ggc tct gat gga att att gat tgt cct ttg ctg ctg	Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu	432		
	130 135 140			
att cag gtg acc tgt ctt aca tgt gga ggt ttc ata ctt gca ttg cgc	Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg	480		
	145 150 155 160			
cta aac cac aca atg tgt gat gca gct gga ttg ctc ttg ttc ctg acc	Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr	528		
	165 170 175			
gcc atc gcg gag atg gca aga ggc gca cat gca cca tct att cta cca	Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro	576		
	180 185 190			
gtg tgg gag aga gag ctc ttg ttc gct cga gat cca cca aga att aca	Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr	624		
	195 200 205			
tgt gct cgt cat gaa tat gaa gac gtg att ggt cat tct gat ggc tca	Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser	672		
	210 215 220			
tac gca tcc agt aac cag tca aac atg gtt caa cga tct ttc tac ttt	Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe	720		
	225 230 235 240			
ggt gcc aag gag atg aga gtc ctt cga aaa cag att cca ccc cac cta	Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu	768		
	245 250 255			

att tcc act tgc tcc aca ttt gac ttg atc aca gct tgt ttg tgg aaa	816
Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys	
260 265 270	
tgt cgc act ctt gca ctt aac att aat cca aaa gag gct gtt cga gtt	864
Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val	
275 280 285	
tca tgc att gtc aat gca cga gga aag cac aac aat gta cgt ctt ccc	912
Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro	
290 295 300	
ttg gga tac tat ggc aat gca ttt gca ttt cca gct gca att tcg aag	960
Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys	
305 310 315 320	
gct gaa cct cta tgc aaa aat cca ctg gga tat gct ttg gag ttg gtg	1008
Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val	
325 330 335	
aag aag gct aaa gct acc atg aat gaa gaa tac tta aga tca gtg gca	1056
Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala	
340 345 350	
gat ctt ttg gta cta aga ggg cga cct caa tat tca tcg aca gga agt	1104
Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser	
355 360 365	
tat tta ata gtt tct gat aat acg cgt gta ggt ttt gga gat gtc aat	1152
Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn	
370 375 380	
ttt gga tgg gga cag ccg gta ttt gct gga ccc gtc aag gcc ttg gat	1200
Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp	
385 390 395 400	
ttg att agc ttc tac gtt caa cac aaa aac aac aca gag gat gga ata	1248
Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile	
405 410 415	
ttg gta cca atg tgt ttg cca tcc tcg gcc atg gag aga ttt cag cag	1296
Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln	
420 425 430	
gaa cta gag agg att act cag gaa cct aag gag gat ata tgt aac aac	1344
Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn	
435 440 445	
ctt aga tca act agt caa tgatgtaagt gttaaagta atgcactttc	1392
Leu Arg Ser Thr Ser Gln	
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tctgaatggt attaaaaaat agccaataat aag	1485
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<213> Musa sp.	
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<221> CDS
 <222> (1)..(1257)
 <223> cDNA

<220>
 <223> Banana alcohol acyl transferase

<400> 12

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ggg gtc acg ccg acg ggc tcg ctc ggc ctc tcc gcc atc gac cgg gtg	96
Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val	
20 25 30	
ccc ggc ctc agg cat atg gtg cgg tcg cta cac gtg ttc agg caa ggc	144
Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly	
35 40 45	
cgg gag ccg gcc agg atc atc agg gaa gca ctg tcg aag gcg ctg gtg	192
Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val	
50 55 60	
aag tac tac ccc ttc gcg ggg cgg ttc gtg gac gat ccc gag ggc ggc	240
Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly	
65 70 75 80	
ggc gag gtt cgt gtc gct tgc act ggc gag ggc gct tgg ttc gtc gag	288
Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu	
85 90 95	
gcc aag gcg gac tgc agc ttg gag gac gtg aag tac ctc gat ctc ccg	336
Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro	
100 105 110	
ctc atg atc cct gag gac gcg ctc ctg ccc aag ccc tgc ccg gga ctg	384
Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu	
115 120 125	
aac ccc ctc gac ctc cct ctc atg ctg cag gtg aca gag ttc gtg ggc	432
Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly	
130 135 140	
ggc gga ttc gtg gtc ggc ctc atc tcc gtc cat acc atc gcc gac ggc	480
Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly	
145 150 155 160	
ctc ggc gtc gtc cag ttc atc aac gcc gtc gcc gag atc gcc cgt ggc	528
Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly	
165 170 175	
ctg ccg aag ccc acc gtg gag cct gca tgg tcc ccg gag gtc ata ccc	576
Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro	
180 185 190	
aac cca cct aag ctg cct ccc ggt ggc ccg ccc gtg ttc ccc tcc ttc	624
Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe	
195 200 205	
aag ctg ctc cac gcc acc gtc gac cta tcc cct gac cac atc gat cac	672
Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His	

210	215	220	
gtc aag tcc cga cac ttg gag ctc acc ggc cag cgc tgc tct acc ttc Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe 225 230 235 240			720
gac gtc gcc atc gcc aac ctg tgg cag tcc cgc acg cgc gcc atc aac Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn 245 250 255			768
ctg gac cca ggc gtc gac gtg cac gtg tgc ttc ttc gcc aac act cgc Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg 260 265 270			816
cac ctg ttg cgc cag gtc gtc ctc ctg ccc ccc gag gat ggc tac tac His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr 275 280 285			864
ggc aac tgc ttc tac ccg gtg acc gcc acc gcc cca agc ggc agg atc Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile 290 295 300			912
gca tcg gcc gag ctc atc gat gtc gtc agc atc atc agg gac gcc aag Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys 305 310 315 320			960
tcg agg ctg ccg ggc gag ttc gcc aag tgg gct gcc ggg gat ttc aag Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys 325 330 335			1008
gac gac cct tac gag ctc agc ttc acg tac aac tcg ctg ttc gtg tcg Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser 340 345 350			1056
gac tgg acc cgg ctc ggc ttc ctc gac gtc gac tac ggc tgg ggc aag Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys 355 360 365			1104
ccc ctc cac gtt ata ccg ttc gcg tac ttg gac atc atg gcg gtc ggc Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly 370 375 380			1152
atc atc ggg gcg ccg ccg gcg ccg caa aag ggg act cgg gtg atg gcg Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala 385 390 395 400			1200
cag tgc gtc gag aag gag cac atg cag gcg ttc ctg gaa gag atg aaa Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys 405 410 415			1248
ggc ttc gct taaaccagca gcagtgtagt acttgtcagt atcc Gly Phe Ala			1291

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 <213> *Fragaria vesca*

<220>
 <221> CDS
 <222> (1)..(1365)
 <223> cDNA

<220>

<223> Strawberry vesca alcohol acyl transferase

<400> 13

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tca act tcc tct tca cca ctt cag cct tac aag ctt acc ctg ctc gac	96
Ser Thr Ser Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp	
20 25 30	
cag ctc act cct cca tcg tat gtc ccc atg gta ttc ttc tac ccc att	144
Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile	
35 40 45	
act ggc cct gca gtc ttc aat ctt caa acc cta gct gac tta aga cat	192
Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His	
50 55 60	
gcc ctt tcc gag act ctc act ttg tac tat cca ctc tct gga agg gtc	240
Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val	
65 70 75 80	
aaa aac aac cta tac atc gat gat ttt gaa gag ggt gtc cca tac ctt	288
Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu	
85 90 95	
gag gct cga gtg aac tgt gac atg aat gat ttt cta agg ctt ccg aaa	336
Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys	
100 105 110	
atc gag tgc cta aat gag ttt gtt cca ata aaa cca ttt agt atg gaa	384
Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu	
115 120 125	
gca ata tct gat gag cgt tac cct ttg ctc gga gtt caa gtt aac att	432
Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile	
130 135 140	
ttc aac tcc gga ata gca atc ggg gtc tcc gtc tct cac aag ctc atc	480
Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile	
145 150 155 160	
gat gga aga act tca gac tgt ttt ctc aag tcg tgg tgt gct gtt ttt	528
Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe	
165 170 175	
cgt ggt tct cgt gac aaa atc ata cat cct aat ctc tct caa gca gca	576
Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala	
180 185 190	
ttg ctt ttc cca cca aga gat gac ttg cct gaa aag tat gcc cgt cag	624
Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln	
195 200 205	
atg gaa ggg tta tgg ttt gtc gga aaa aaa gtt gct aca agg aga ttt	672
Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe	
210 215 220	
gta ttt ggt gcg aaa gcc ata tct gta att caa gat gaa gca aag agc	720
Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser	

225	230	235	240	
gag tcc gtg ccc aag cca tca cga gtt	cag gct gtc act agt ttt ctc			768
Glu Ser Val Pro Lys 245	Gln Ala Val Thr Ser Phe Leu 255			
tgg aaa cat cta atc gct act tct cgg	gca cta aca tca ggt act act			816
Trp Lys His Leu Ile Ala Thr Ser Arg 265	Ala Leu Thr Ser Gly Thr Thr 270			
tca aca aga ctt tct ata gca acc cag	gta gtg aac ata aga tca cgg			864
Ser Thr Arg Leu Ser Ile Ala Thr Gln 280	Val Val Asn Ile Arg Ser Arg 285			
agg aac atg gag aca gtg tgg gat aat gcc	att gga aac ttg ata tgg			912
Arg Asn Met Glu Thr Val Trp 295	Ile Gly Asn Leu Ile Trp 300			
ttc gct ccg gcc ata cta gag cta agt cat	aca aca cta gag atc agt			960
Phe Ala Pro Ala Ile Leu Glu Leu Ser His 310	Thr Thr Leu Glu Ile Ser 320			
gat ctt aag ctg tgt gac ttg gtt aac ttg	ctc aat gga tct gtc aaa			1008
Asp Leu Lys Leu Cys Asp Leu Val Asn Leu 330	Leu Leu Asn Gly Ser Val Lys 335			
caa tgt aac ggt gat tac ttt gag act ttc	atg ggt aaa gag gga tat			1056
Gln Cys Asn Gly Asp Tyr Phe Glu Thr 345	Met Gly Lys Glu Gly Tyr 350			
gga agc atg tgc gag tat cta gat ttt cag	agg act atg agt tct atg			1104
Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met 365				
gaa cca gca cca gag att tat tta ttc acg	agc tgg act aat ttt ttc			1152
Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp 380	Thr Thr Asn Phe Phe 385			
aac caa ctt gat ttt gga tgg ggg agg aca	tca tgg att gga gtt gca			1200
Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp 395	Ile Gly Val Ala 400			
gga aaa att gaa tct gca ttt tgc aat ctc	aca aca tta gtt cca aca			1248
Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr 415				
cca tgc gat act gga att gaa gcg tgg gtg	aat cta gaa gaa gaa aaa			1296
Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys 425				
atg gct atg cta gaa caa gat ccc cag ttt	cta gca cta gca tct cca			1344
Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro 445				
aag acg cta att tca aga tat tgattaagga	agattatgcg gctcgtgcaa			1395
Lys Thr Leu Ile Ser Arg Tyr 455				
tgtttccatt ttgttgtgat taaggcttaa attagttcac	cagccaatca ataagatgca			1455
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<210> 14
 <211> 434
 <212> PRT
 <213> Citrus limon
 <223> Citrus limon alcohol acyl transferase

<400> 14

Met	Lys	Ile	His	Val	Lys	Glu	Ser	Thr	Ile	Ile	Arg	Pro	Ala	Gln	Glu
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Thr	Pro	Lys	His	Arg	Leu	Gln	Ile	Ser	Asp	Leu	Asp	Met	Ile	Val	Pro
			20					25					30		
Ser	Asn	Tyr	Val	Pro	Ser	Val	Tyr	Phe	Tyr	Arg	Arg	Ser	Ser	Asp	Cys
		35					40					45			
Thr	Asp	Phe	Phe	Glu	Val	Gly	Leu	Leu	Lys	Lys	Ala	Leu	Ser	Glu	Val
	50					55					60				
Leu	Val	Pro	Phe	Tyr	Pro	Val	Ala	Gly	Arg	Leu	Gln	Lys	Asp	Glu	Asn
	65				70					75					80
Arg	Lys	Ile	Glu	Ile	Leu	Cys	Asn	Gly	Glu	Gly	Val	Leu	Phe	Leu	Glu
				85					90						95
Ala	Glu	Thr	Ser	Cys	Gly	Ile	Asp	Asp	Phe	Gly	Asp	Phe	Ser	Gln	Gly
			100					105					110		
Ser	Lys	Leu	Leu	Thr	Leu	Val	Pro	Thr	Val	Gly	Asp	Thr	Lys	Asp	Ile
		115					120					125			
Ser	Ser	His	Pro	Leu	Leu	Met	Ala	Gln	Val	Thr	Tyr	Phe	Lys	Cys	Gly
	130					135					140				
Gly	Val	Cys	Val	Gly	Thr	Arg	Val	Asn	His	Thr	Leu	Val	Asp	Gly	Ala
145					150					155					160
Ser	Ala	Tyr	His	Ile	Ile	Asn	Ser	Trp	Ala	Glu	Thr	Thr	Arg	Gly	Val
				165					170					175	
Pro	Ile	Ser	Thr	Gln	Pro	Phe	Tyr	Asp	Arg	Thr	Ile	Leu	Ser	Val	Gly
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		195					200					205			
Ser	Met	Asn	Ala	Pro	Pro	Thr	Gln	Asn	Pro	Glu	Ile	Ile	Ser	Thr	Ala
	210					215					220				
Ile	Leu	Asn	Leu	Ser	Leu	Asp	Gln	Ile	His	Thr	Leu	Lys	Glu	Lys	Ser
225					230					235					240
Lys	Thr	Asp	His	Glu	Pro	Asn	Val	Lys	Tyr	Ser	Arg	Met	Ala	Ile	Leu
				245					250					255	
Ala	Ala	His	Ile	Trp	Arg	Ser	Met	Cys	Lys	Ala	Arg	Gly	Leu	Ser	Asp
			260					265					270		
Asp	Gln	Val	Ser	Lys	Leu	His	Phe	Pro	Thr	Asp	Gly	Arg	Gln	Arg	Leu
		275					280					285			
Asn	Pro	Pro	Leu	Pro	Pro	Gly	Tyr	Phe	Gly	Asn	Val	Ile	Phe	Thr	Thr

290	295	300
Ser 305 Leu Thr Ala Ser 310 Ser Gly Asp Ile Leu Ser 315 Glu Pro Leu Asn His 320		
Thr Val Glu Arg 325 Ile Gln Lys Ala Leu Lys 330 Arg Met Asp Asp Glu Tyr 335		
Leu Lys Ser 340 Ala Leu Ala Tyr Leu Lys 345 Gln Gln Pro Asp Leu Asn Ala 350		
Leu Arg Lys 355 Gly Gly His Ile Tyr 360 Lys Cys Pro Asn Leu Asn Ile Val 365		
Asn 370 Leu Ala Asn Met Pro 375 Met Tyr Val Ala Asn 380 Phe Gly Trp Gly Gln 385		
Pro Ile Phe Ala Arg 390 Ile Val Asn Thr Tyr 395 Tyr Glu Gly Ile Ala His 400		
Ile Tyr Pro Ser 405 Pro Ser Asn Asp Gly Thr 410 Leu Ser Val Val Ile Asn 415		
Ser Val Ala Asp 420 His Met Gln Leu Phe 425 Lys Lys Phe Phe Tyr 430 Glu Ile 435		

Phe Asp

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 <213> Mangifera indica

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 <223> cDNA

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Met Ile Ile Thr Val Lys Glu Ser Thr Met Val Pro Pro Ser Ala Glu	
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acg ccg agg ata tct ctg tgg aac tcc aac gcc gat ctg gtg gtt ccc	96
Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro	
20 25 30	
cga ttt cat act ccc agc gtt tac ttc tac cgg ccc acc ggg gcc ata	144
Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile	
35 40 45	
aac ttc ttt gat ggt aag ttg ctc aag gag gct ctc ggc aag gct ctg	192
Asn Phe Phe Asp Gly Lys Leu Leu Lys Glu Ala Leu Gly Lys Ala Leu	
50 55 60	
gtg ccg ttc tac cca atg gcg ggg cgg tta aag cgt gac gaa gat gga	240
Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly	
65 70 75 80	

agg att gag atc gat tgt aat gct gaa ggc gtc ttg ttt gtt gag gcc	288
Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala	
85 90 95	
gaa act ccc tct gtt att gat gat ttt ggt gac ttt gcg ccc act tta	336
Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu	
100 105 110	
gag ctc aag cag ctc att ccg aca gtg gat tac tcc ggc ggg atc tct	384
Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser	
115 120 125	
acg tat ccc cta ttg gcg tta cag gtt act cac ttc aaa tgt ggt gga	432
Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly	
130 135 140	
gtt tca ctt ggt gta ggt atg caa cac cat gcg gca gat gga ttt tct	480
Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser	
145 150 155 160	
ggt ctt cac ttt gta aac aca tgg tca gac att gct cgt ggt ctt gat	528
Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp	
165 170 175	
gtt aac atc acc ctg ttc att gac cgg act ctg ctc aga gca cag gat	576
Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp	
180 185 190	
ccc cct cag cct act ttc cca cac aca tgg aat acc agg ccg cct cct	624
Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro	
195 200 205	
tcc ctg aaa act cct cca cca gca gtt tct gag cct act gct gtc tcc	672
Ser Leu Lys Thr Pro Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser	
210 215 220	
att ttt aag ttg acg cgg gac cag ctc aac atc ctc aaa gcc aag gcc	720
Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala	
225 230 235 240	
aaa gaa gat ggt aac act atc aac tat agc tca tat gag atg ctg gcg	768
Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala	
245 250 255	
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Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp	
260 265 270	
caa gag act aaa ttg tac ata gca act gac gga cgt gct aga tta atc	864
Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile	
275 280 285	
ccc cca ctt cca cct ggt tac ttt ggg aat gtg ata ttt aca gcc aca	912
Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr	
290 295 300	
cca atg gca gta gca ggt gat ctc cag tca aag cct ata tgg tat gct	960
Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala	
305 310 315 320	
gct ggc cag att cat gat gcc ttg gtt cga atg gac aac gac tat tta	1008
Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu	

	325	330	335	
agg tca gcc ctc gat tac cta gag ctt cag cct gat tta tca gca tta				1056
Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu				
	340	345	350	
ggt cgt ggt gcc cat aca ttt agg tgt cca aat ctc ggg att act agt				1104
Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser				
	355	360	365	
tgg gtt aga ctg cca ata cat gat gca gat ttt ggt tgg ggt cca ccc				1152
Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro				
	370	375	380	
aca ttt atg ggg cct ggt ggg att gca tat gaa ggc tta tca ttt gta				1200
Thr Phe Met Gly Pro Gly Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val				
	385	390	395	400
ttg cca agc cct aca aat gat ggg agc tta tca gtt gcc atc tct cta				1248
Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu				
	405	410	415	
caa tct gaa cac atg aaa ctg ttt cag aag ttc ttt tat gat att taa				1296
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acc gaa atc atc aag cct tct tcg ccg acg cct caa cac caa agt acc				102
Thr Glu Ile Ile Lys Pro Ser Ser Pro Thr Pro Gln His Gln Ser Thr				
	10	15	20	
tat aaa ctt tca att att gat caa tta act cct aat gtt tac ttt tcc				150
Tyr Lys Leu Ser Ile Ile Asp Gln Leu Thr Pro Asn Val Tyr Phe Ser				
	25	30	35	
atc att ctc ttg tat tca aaa gct ggt gaa agt acc gcc aaa act tca				198
Ile Ile Leu Leu Tyr Ser Lys Ala Gly Glu Ser Thr Ala Lys Thr Ser				
	40	45	50	55
gat cac ctc aaa gaa tct ctt tca aat aca tta acc cac tac tat cct				246
Asp His Leu Lys Glu Ser Leu Ser Asn Thr Leu Thr His Tyr Tyr Pro				
	60	65	70	
tta gct ggg caa ctc aaa tat gat caa ctt att gtt gat tgt aac gac				294
Leu Ala Gly Gln Leu Lys Tyr Asp Gln Leu Ile Val Asp Cys Asn Asp				

75										80					85					
caa	ggt	gtc	ccg	ttc	atc	gaa	gca	cac	gtc	acc	aac	gac	atg	cgt	cag	342				
Gln	Gly	Val	Pro	Phe	Ile	Glu	Ala	His	Val	Thr	Asn	Asp	Met	Arg	Gln					
		90					95					100								
ctt	ctt	aaa	ata	cca	aat	att	gat	gtt	ctc	gaa	caa	ctc	cta	cca	ttc	390				
Leu	Leu	Lys	Ile	Pro	Asn	Ile	Asp	Val	Leu	Glu	Gln	Leu	Leu	Pro	Phe					
	105					110					115									
aaa	ccg	cat	gag	ggt	ttt	gat	tct	gat	cgt	tcc	aac	cta	acc	gtt	cag	438				
Lys	Pro	His	Glu	Gly	Phe	Asp	Ser	Asp	Arg	Ser	Asn	Leu	Thr	Val	Gln					
120					125					130					135					
gtc	aat	tac	ttt	ggt	tgt	gaa	gga	atg	gcg	att	ggt	ctg	tgc	ttc	aga	486				
Val	Asn	Tyr	Phe	Gly	Cys	Glu	Gly	Met	Ala	Ile	Gly	Leu	Cys	Phe	Arg					
			140						145					150						
cac	aaa	gtt	att	gat	gca	aca	acg	gct	gca	ttc	ttt	gtt	aag	aac	tgg	534				
His	Lys	Val	Ile	Asp	Ala	Thr	Thr	Ala	Ala	Phe	Phe	Val	Lys	Asn	Trp					
		155						160					165							
ggt	gta	att	gct	cgt	ggt	gct	gga	gaa	att	aag	gac	gtg	atc	att	gat	582				
Gly	Val	Ile	Ala	Arg	Gly	Ala	Gly	Glu	Ile	Lys	Asp	Val	Ile	Ile	Asp					
	170					175						180								
cat	gct	tcc	ctg	ttt	ccc	gca	aga	gat	tta	tcg	tgc	tta	aca	aag	agt	630				
His	Ala	Ser	Leu	Phe	Pro	Ala	Arg	Asp	Leu	Ser	Cys	Leu	Thr	Lys	Ser					
	185					190					195									
gtt	gac	gaa	gag	ttt	ttg	aag	cca	gag	tct	gaa	aca	aag	cgc	ttt	gtg	678				
Val	Asp	Glu	Glu	Phe	Leu	Lys	Pro	Glu	Ser	Glu	Thr	Lys	Arg	Phe	Val					
200					205					210					215					
ttt	gat	ggt	gcc	act	ata	gct	tct	tta	caa	gaa	acg	ttt	gca	agt	ttt	726				
Phe	Asp	Gly	Ala	Thr	Ile	Ala	Ser	Leu	Gln	Glu	Thr	Phe	Ala	Ser	Phe					
			220						225					230						
gaa	cga	cgt	cca	aca	cgc	ttt	gag	gtt	gtg	tca	gca	gtt	att	ttg	ggt	774				
Glu	Arg	Arg	Pro	Thr	Arg	Phe	Glu	Val	Val	Ser	Ala	Val	Ile	Leu	Gly					
			235				240						245							
gct	ttg	ata	act	gca	acg	aga	gaa	tct	gat	gat	gag	tct	aac	gtt	cct	822				
Ala	Leu	Ile	Thr	Ala	Thr	Arg	Glu	Ser	Asp	Asp	Glu	Ser	Asn	Val	Pro					
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gaa	cgt	ttg	gac	acg	ata	att	tca	gtg	aat	cta	cgg	cag	aga	atg	aat	870				
Glu	Arg	Leu	Asp	Thr	Ile	Ile	Ser	Val	Asn	Leu	Arg	Gln	Arg	Met	Asn					
	265					270					275									
cca	cca	ttc	ccg	gag	cat	tgc	atg	ggg	aat	ata	ata	tcc	ggg	gga	tta	918				
Pro	Pro	Phe	Pro	Glu	His	Cys	Met	Gly	Asn	Ile	Ile	Ser	Gly	Gly	Leu					
280					285					290					295					
gtg	tat	tgg	cca	ctg	gag	aaa	aaa	gtt	gat	tac	ggg	tgt	tta	gca	aaa	966				
Val	Tyr	Trp	Pro	Leu	Glu	Lys	Lys	Val	Asp	Tyr	Gly	Cys	Leu	Ala	Lys					
			300						305					310						
gag	att	cat	gaa	tca	ata	aag	aaa	gtg	gac	gat	caa	ttt	gcg	agg	aag	1014				
Glu	Ile	His	Glu	Ser	Ile	Lys	Lys	Val	Asp	Asp	Gln	Phe	Ala	Arg	Lys					
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Phe Tyr Gly Asp Ala Glu Phe Leu Asn Leu Pro Arg Leu Ala Gly Ala	
330 335 340	
gag gat gtg aag aag cgg gag ttt tgg gtt act agt tgg tgc aaa act	1110
Glu Asp Val Lys Lys Arg Glu Phe Trp Val Thr Ser Trp Cys Lys Thr	
345 350 355	
ccg ctg tat gaa gct gat ttc ggg tgg ggg aat cct aag tgg gca ggc	1158
Pro Leu Tyr Glu Ala Asp Phe Gly Trp Gly Asn Pro Lys Trp Ala Gly	
360 365 370 375	
aac tcc atg agg ctt aat cag att act gtt ttc ttt gac agt agt gat	1206
Asn Ser Met Arg Leu Asn Gln Ile Thr Val Phe Phe Asp Ser Ser Asp	
380 385 390	
ggt gag gga gtt gaa gct tgg gtg ggg ttg ccc aga aaa gac atg gct	1254
Gly Glu Gly Val Glu Ala Trp Val Gly Leu Pro Arg Lys Asp Met Ala	
395 400 405	
cga ttt gaa aaa gat tct ggc atc ctt gct tac act tcc cct aat cca	1302
Arg Phe Glu Lys Asp Ser Gly Ile Leu Ala Tyr Thr Ser Pro Asn Pro	
410 415 420	
agc ata ttt tgagggttta tttatttttt attgcactgt ttgttatttg	1351
Ser Ile Phe	
425	
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<220>
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Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr Lys Val	
5 10 15	
acc cct ttc gtc aac ccc aac tca aag acg acg tcg ttt act ctc gat	153
Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr Leu Asp	
20 25 30	
ctc acc tat ttc gac ttt ttc tgg ttc aag aat cct cct gtg gaa cgc	201
Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val Glu Arg	
35 40 45 50	

ctc ttc ttc tat gag atg act gac ttg acg tgg gat tta ttc aac tcg	249
Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe Asn Ser	
55 60 65	
gag atc ctc cca aag ctg aag cac tcc ctt tcc ttc act ctc ctt cat	297
Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu Leu His	
70 75 80	
tac ctc cct ctt gct ggt cac atc atg tgg ccg ctg gat gcc gca aag	345
Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala Ala Lys	
85 90 95	
cct gcc gtc tac tac ttt ccc gac caa aac gac ggc gtt tca ttc gca	393
Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser Phe Ala	
100 105 110	
gtt gct gag tgg tct tcc gag tgc cac gca ggc ttc cat cac ctc tcc	441
Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His Leu Ser	
115 120 125 130	
ggc aac gga atc cgc caa gca gtt gaa ttt cat cct ctt gtg ccc cag	489
Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val Pro Gln	
135 140 145	
ttg tcg ctt acg gac gat aaa gct gag gta att gcc atc caa ata aca	537
Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln Ile Thr	
150 155 160	
ctg ttt ccg aat caa ggc ttc tca att ggt gtt tca tct cac cat gca	585
Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His His Ala	
165 170 175	
att ctt gat gga aaa act tcg acc ttg ttc ctg aaa tct tgg gct tat	633
Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp Ala Tyr	
180 185 190	
ttg tgc aaa caa tta caa tta tgc cat cac cct tgt ttg tca cct gaa	681
Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser Pro Glu	
195 200 205 210	
cta acc cct ctt ctc gac cgg act gtc atc aaa gat ccg aca ggt cag	729
Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr Gly Gln	
215 220 225	
gac atg ctg caa ctg aat aag tgg gtt gtc ggg tcg gat aat tcg gat	777
Asp Met Leu Gln Leu Asn Lys Trp Val Val Gly Ser Asp Asn Ser Asp	
230 235 240	
ccc cag aag ata cgg agc ttg aag gtt tta cca ttc tta gac tct gag	825
Pro Gln Lys Ile Arg Ser Leu Lys Val Leu Pro Phe Leu Asp Ser Glu	
245 250 255	
tct ctg aac aaa ttg gtc cga gcc aca ttt gag ttg acg cgt gaa gat	873
Ser Leu Asn Lys Leu Val Arg Ala Thr Phe Glu Leu Thr Arg Glu Asp	
260 265 270	
att acg aaa ctc agg cac aag gtt aat cat cag tta tca aaa tca tca	921
Ile Thr Lys Leu Arg His Lys Val Asn His Gln Leu Ser Lys Ser Ser	
275 280 285 290	
aaa tca aag caa gtt cgt tta tca act ttt gtg ctt aca tta gct tat	969
Lys Ser Lys Gln Val Arg Leu Ser Thr Phe Val Leu Thr Leu Ala Tyr	

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gct	gaa	gct	gca	gca	ggg	aat	gat	gaa	att	aaa	aat	att	att	gtg	gga	1065				
Ala	Glu	Ala	Ala	Ala	Gly	Asn	Asp	Glu	Ile	Lys	Asn	Ile	Ile	Val	Gly					
		325					330					335								
ttc	act	gcg	gat	tat	agg	agc	cgt	ttg	gat	cct	cca	att	cca	ctt	aat	1113				
Phe	Thr	Ala	Asp	Tyr	Arg	Ser	Arg	Leu	Asp	Pro	Pro	Ile	Pro	Leu	Asn					
	340					345					350									
tat	ttt	ggg	aac	tgc	aat	ggg	aga	cat	tgt	gag	act	gca	aaa	gca	agt	1161				
Tyr	Phe	Gly	Asn	Cys	Asn	Gly	Arg	His	Cys	Glu	Thr	Ala	Lys	Ala	Ser					
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gat	ttc	gtt	caa	gaa	aat	ggg	gtt	gct	ttt	gtt	gca	gag	atg	tta	agt	1209				
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gat	atg	gtc	aaa	ggg	atc	gat	gcg	gat	gcc	att	gaa	gcc	aat	gat	gat	1257				
Asp	Met	Val	Lys	Gly	Ile	Asp	Ala	Asp	Ala	Ile	Glu	Ala	Asn	Asp	Asp					
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Lys	Val	Ser	Glu	Ile	Leu	Glu	Ile	Leu	Lys	Glu	Gly	Ala	Met	Ile	Phe					
	405						410					415								
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Ser	Val	Ala	Gly	Ser	Thr	Gln	Phe	Asp	Val	Tyr	Gly	Ser	Asp	Phe	Gly					
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Trp	Gly	Arg	Pro	Lys	Lys	Val	Glu	Ile	Val	Ser	Ile	Asp	Arg	Thr	Gln					
435					440					445					450					
gcc	atc	tct	ttg	gca	gag	aga	aga	gat	gga	gga	ggc	ggc	gtt	gag	gtt	1449				
Ala	Ile	Ser	Leu	Ala	Glu	Arg	Arg	Asp	Gly	Gly	Gly	Gly	Val	Glu	Val					
				455					460					465						
gga	gtt	gtt	tta	gag	aag	caa	caa	atg	gag	gtt	ttt	gaa	tct	gta	ttt	1497				
Gly	Val	Val	Leu	Glu	Lys	Gln	Gln	Met	Glu	Val	Phe	Glu	Ser	Val	Phe					
			470					475					480							
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Ala	Asp	Gly	Leu	Lys	Asn	Asp	Leu	Val												
		485					490													
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cct tct gag cca acc cca tct acg gtt ttg tct ctc tca gct ctt gat	96
Pro Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp	
20 25 30	
tct cag ctt ttc ttg cgt ttc act att gag tat ctc ttg gtc tat aga	144
Ser Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg	
35 40 45	
cct cgc cct ggt ttg gac cca ctt gct acc gtg gct cgt gtc aag tcc	192
Pro Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser	
50 55 60	
gca ctc gcc aaa gcc ttg gtt cct tac tat ccc ctc gcg ggt cgg gtc	240
Ala Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val	
65 70 75	
aga gct aaa caa gac ggg tcg ggc tta ttg gaa gtc gtg tgt cta ggc	288
Arg Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly	
80 85 90 95	
caa ggc gct gtg ttc atc gaa gcc gtc gac cgt gaa agt acg atc acc	336
Gln Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr	
100 105 110	
gat ttt gag agt gct ccc agg tat gtt act cag tgg agg aaa ctg ctg	384
Asp Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu	
115 120 125	
tcg tta tac gtg gcg gat gtt ctc aaa ggg gcc cca cct ctt gtc gtt	432
Ser Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val	
130 135 140	
cag ctg act tgg ctt aga gat gga gcc gca gcg ctc ggt att ggc ttt	480
Gln Leu Thr Trp Leu Arg Asp Gly Ala Ala Ala Leu Gly Ile Gly Phe	
145 150 155	
aac cat tgt gtt tgc gat ggt atc ggc agc gcc gag ttc ctc aac ttg	528
Asn His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu	
160 165 170 175	
ttt act gag tta tgt acg agc cgt cat aac gaa ctg ggt ggt ggc cat	576
Phe Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly Gly His	
180 185 190	
tct ctg ccg aaa ccc gtt tgg gat cgc cac cta atg aac tcc tcc tca	624
Ser Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser	
195 200 205	
tca cgt caa cag cat gca gat aca cgt gcc agc tca gtg agt cac ctg	672
Ser Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu	
210 215 220	

gaa ttc aac aga gtg gct gat ctt tgt ggt ttt gtt tct cgt ttt tcc	720
Glu Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser	
225 230 235	
aac gaa agg ctt gtt ccc act tca ata acg ttc gat aaa cga cgc tta	768
Asn Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu	
240 245 250 255	
aac gag ctg cgg aag ctg gct ctg tcc acg agt cga ccc agt gag ctg	816
Asn Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu	
260 265 270	
gct tac acg tca ttt gaa gtt ctt tca gct cat gtg tgg aga agc tgg	864
Ala Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp	
275 280 285	
gct agg tcg ttg aat ctt ccg tcg aat caa atc ttg aag ctt cta ttt	912
Ala Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe	
290 295 300	
agc atc aat gta cgt aac cgt gtc aag ccg agt ctc ccc agt ggc tat	960
Ser Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr	
305 310 315	
tat ggc gat gca ttt gta tta ggc tgt gct caa acg agg gtt aaa gat	1008
Tyr Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp	
320 325 330 335	
ttg aca gag aag gac tta ggg cat gca gca atg ttg gtt aaa aag gcg	1056
Leu Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala	
340 345 350	
aaa gag aga gtt gat agt gag tat gtg aag tcg gtc atc gac tca gtg	1104
Lys Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val	
355 360 365	
agt cac acg aga gcg tgt ccc gac tca gtc ggg gtg ttg ata gtg tcg	1152
Ser His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser	
370 375 380	
cag tgg tca agg cta ggg tta gag aga gtt gac ttt ggg atg ggg agg	1200
Gln Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg	
385 390 395	
ccg act caa gtg ggt ccc att tgc tgc gac agg tat tgc ctg ttt cta	1248
Pro Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu	
400 405 410 415	
ccg gtt ttc aat cag acg gac gct gtt aag gtg atg gtg gcg gtc ccc	1296
Pro Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro	
420 425 430	
aca agt gca gtt gac aag tat gag cat ctc gcg aag ggc tta tgc tgg	1344
Thr Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp	
435 440 445	
tgaggaccac accgcatgat gacccaccca tgtaatacgt tgacttataa actcagtttg	1404
actttttaact tttttaacaa gtgatggaat ttcagtgatt gactcatcac tttgatcctg	1464
atccaataaaa taattgaatt gagttcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa	1520

<210> 19
 <211> 455
 <212> PRT
 <213> *Fragaria vesca*
 <223> Strawberry vesca alcohol acyl transferase

<400> 19

Met	Glu	Lys	Ile	Glu	Val	Ser	Ile	Ile	Ser	Lys	His	Thr	Ile	Lys	Pro
1				5					10					15	
Ser	Thr	Ser	Ser	Ser	Pro	Leu	Gln	Pro	Tyr	Lys	Leu	Thr	Leu	Leu	Asp
			20					25					30		
Gln	Leu	Thr	Pro	Pro	Ser	Tyr	Val	Pro	Met	Val	Phe	Phe	Tyr	Pro	Ile
		35					40					45			
Thr	Gly	Pro	Ala	Val	Phe	Asn	Leu	Gln	Thr	Leu	Ala	Asp	Leu	Arg	His
	50					55					60				
Ala	Leu	Ser	Glu	Thr	Leu	Thr	Leu	Tyr	Tyr	Pro	Leu	Ser	Gly	Arg	Val
65					70					75					80
Lys	Asn	Asn	Leu	Tyr	Ile	Asp	Asp	Phe	Glu	Glu	Gly	Val	Pro	Tyr	Leu
				85					90					95	
Glu	Ala	Arg	Val	Asn	Cys	Asp	Met	Asn	Asp	Phe	Leu	Arg	Leu	Pro	Lys
			100					105					110		
Ile	Glu	Cys	Leu	Asn	Glu	Phe	Val	Pro	Ile	Lys	Pro	Phe	Ser	Met	Glu
		115					120					125			
Ala	Ile	Ser	Asp	Glu	Arg	Tyr	Pro	Leu	Leu	Gly	Val	Gln	Val	Asn	Ile
	130					135					140				
Phe	Asn	Ser	Gly	Ile	Ala	Ile	Gly	Val	Ser	Val	Ser	His	Lys	Leu	Ile
145					150					155					160
Asp	Gly	Arg	Thr	Ser	Asp	Cys	Phe	Leu	Lys	Ser	Trp	Cys	Ala	Val	Phe
				165					170					175	
Arg	Gly	Ser	Arg	Asp	Lys	Ile	Ile	His	Pro	Asn	Leu	Ser	Gln	Ala	Ala
			180					185					190		
Leu	Leu	Phe	Pro	Pro	Arg	Asp	Asp	Leu	Pro	Glu	Lys	Tyr	Ala	Arg	Gln
		195					200					205			
Met	Glu	Gly	Leu	Trp	Phe	Val	Gly	Lys	Lys	Val	Ala	Thr	Arg	Arg	Phe
	210					215					220				
Val	Phe	Gly	Ala	Lys	Ala	Ile	Ser	Val	Ile	Gln	Asp	Glu	Ala	Lys	Ser
225					230					235					240
Glu	Ser	Val	Pro	Lys	Pro	Ser	Arg	Val	Gln	Ala	Val	Thr	Ser	Phe	Leu
				245					250					255	
Trp	Lys	His	Leu	Ile	Ala	Thr	Ser	Arg	Ala	Leu	Thr	Ser	Gly	Thr	Thr
			260					265					270		
Ser	Thr	Arg	Leu	Ser	Ile	Ala	Thr	Gln	Val	Val	Asn	Ile	Arg	Ser	Arg
		275					280					285			
Arg	Asn	Met	Glu	Thr	Val	Trp	Asp	Asn	Ala	Ile	Gly	Asn	Leu	Ile	Trp

290	295	300
Phe Ala Pro Ala Ile Leu Glu Leu Ser His Thr Thr Leu Glu Ile Ser 305 310 315 320		
Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys 325 330 335		
Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr 340 345 350		
Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met 355 360 365		
Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe 370 375 380		
Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala 385 390 395 400		
Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr 405 410 415		
Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys 420 425 430		
Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro 435 440 445		
Lys Thr Leu Ile Ser Arg Tyr 450 455		

<210> 20
 <211> 419
 <212> PRT
 <213> Musa sp.
 <223> Banana alcohol acyl transferase

<400> 20
Met Ser Phe Ala Val Thr Arg Thr Ser Arg Ser Leu Val Thr Pro Cys 1 5 10 15
Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val 20 25 30
Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly 35 40 45
Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val 50 55 60
Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly 65 70 75 80
Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu 85 90 95
Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro 100 105 110
Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu 115 120 125

Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly
 130 135 140
 Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly
 145 150 155 160
 Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly
 165 170 175
 Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro
 180 185 190
 Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe
 195 200 205
 Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His
 210 215 220
 Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe
 225 230 235 240
 Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn
 245 250 255
 Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg
 260 265 270
 His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr
 275 280 285
 Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile
 290 295 300
 Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys
 305 310 315 320
 Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys
 325 330 335
 Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser
 340 345 350
 Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys
 355 360 365
 Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly
 370 375 380
 Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala
 385 390 395 400
 Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys
 405 410 415

Gly Phe Ala

<210> 21
 <211> 454
 <212> PRT
 <213> Malus sp.
 <223> Apple alcohol acyl transferase

<400> 21

Met	Ser	Phe	Ser	Val	Leu	Gln	Val	Lys	Arg	Leu	Gln	Pro	Glu	Leu	Ile
1				5					10					15	
Thr	Pro	Ala	Lys	Ser	Thr	Pro	Gln	Glu	Thr	Lys	Phe	Leu	Ser	Asp	Ile
			20					25					30		
Asp	Asp	Gln	Glu	Ser	Leu	Arg	Val	Gln	Ile	Pro	Ile	Ile	Met	Cys	Tyr
		35					40					45			
Lys	Asp	Asn	Pro	Ser	Leu	Asn	Lys	Asn	Arg	Asn	Pro	Val	Lys	Ala	Ile
	50					55					60				
Arg	Glu	Ala	Leu	Ser	Arg	Ala	Leu	Val	Tyr	Tyr	Tyr	Pro	Leu	Ala	Gly
	65				70					75					80
Arg	Leu	Arg	Glu	Gly	Pro	Asn	Arg	Lys	Leu	Val	Val	Asp	Cys	Asn	Gly
				85					90					95	
Glu	Gly	Ile	Leu	Phe	Val	Glu	Ala	Ser	Ala	Asp	Val	Thr	Leu	Glu	Gln
			100					105					110		
Leu	Gly	Asp	Lys	Ile	Leu	Pro	Pro	Cys	Pro	Leu	Leu	Glu	Glu	Phe	Leu
		115					120					125			
Tyr	Asn	Phe	Pro	Gly	Ser	Asp	Gly	Ile	Ile	Asp	Cys	Pro	Leu	Leu	Leu
	130					135					140				
Ile	Gln	Val	Thr	Cys	Leu	Thr	Cys	Gly	Gly	Phe	Ile	Leu	Ala	Leu	Arg
145					150					155					160
Leu	Asn	His	Thr	Met	Cys	Asp	Ala	Ala	Gly	Leu	Leu	Leu	Phe	Leu	Thr
				165					170					175	
Ala	Ile	Ala	Glu	Met	Ala	Arg	Gly	Ala	His	Ala	Pro	Ser	Ile	Leu	Pro
			180					185					190		
Val	Trp	Glu	Arg	Glu	Leu	Leu	Phe	Ala	Arg	Asp	Pro	Pro	Arg	Ile	Thr
		195					200					205			
Cys	Ala	Arg	His	Glu	Tyr	Glu	Asp	Val	Ile	Gly	His	Ser	Asp	Gly	Ser
	210					215					220				
Tyr	Ala	Ser	Ser	Asn	Gln	Ser	Asn	Met	Val	Gln	Arg	Ser	Phe	Tyr	Phe
225				230						235					240
Gly	Ala	Lys	Glu	Met	Arg	Val	Leu	Arg	Lys	Gln	Ile	Pro	Pro	His	Leu
				245					250					255	
Ile	Ser	Thr	Cys	Ser	Thr	Phe	Asp	Leu	Ile	Thr	Ala	Cys	Leu	Trp	Lys
			260					265					270		
Cys	Arg	Thr	Leu	Ala	Leu	Asn	Ile	Asn	Pro	Lys	Glu	Ala	Val	Arg	Val
		275					280					285			
Ser	Cys	Ile	Val	Asn	Ala	Arg	Gly	Lys	His	Asn	Asn	Val	Arg	Leu	Pro
	290					295					300				
Leu	Gly	Tyr	Tyr	Gly	Asn	Ala	Phe	Ala	Phe	Pro	Ala	Ala	Ile	Ser	Lys
305					310					315					320
Ala	Glu	Pro	Leu	Cys	Lys	Asn	Pro	Leu	Gly	Tyr	Ala	Leu	Glu	Leu	Val

				325						330						335			
Lys	Lys	Ala	Lys	Ala	Thr	Met	Asn	Glu	Glu	Tyr	Leu	Arg	Ser	Val	Ala				
			340					345					350						
Asp	Leu	Leu	Val	Leu	Arg	Gly	Arg	Pro	Gln	Tyr	Ser	Ser	Thr	Gly	Ser				
		355					360					365							
Tyr	Leu	Ile	Val	Ser	Asp	Asn	Thr	Arg	Val	Gly	Phe	Gly	Asp	Val	Asn				
	370					375					380								
Phe	Gly	Trp	Gly	Gln	Pro	Val	Phe	Ala	Gly	Pro	Val	Lys	Ala	Leu	Asp				
385					390					395					400				
Leu	Ile	Ser	Phe	Tyr	Val	Gln	His	Lys	Asn	Asn	Thr	Glu	Asp	Gly	Ile				
				405					410					415					
Leu	Val	Pro	Met	Cys	Leu	Pro	Ser	Ser	Ala	Met	Glu	Arg	Phe	Gln	Gln				
			420					425					430						
Glu	Leu	Glu	Arg	Ile	Thr	Gln	Glu	Pro	Lys	Glu	Asp	Ile	Cys	Asn	Asn				
	435						440					445							
Leu	Arg	Ser	Thr	Ser	Gln														
	450																		
<210>	22																		
<211>	431																		
<212>	PRT																		
<213>	Mangifera indica																		
<223>	Mango alcohol acyl transferase																		
<400>	22																		
Met	Ile	Ile	Thr	Val	Lys	Glu	Ser	Thr	Met	Val	Pro	Pro	Ser	Ala	Glu				
1				5					10					15					
Thr	Pro	Arg	Ile	Ser	Leu	Trp	Asn	Ser	Asn	Ala	Asp	Leu	Val	Val	Pro				
			20					25					30						
Arg	Phe	His	Thr	Pro	Ser	Val	Tyr	Phe	Tyr	Arg	Pro	Thr	Gly	Ala	Ile				
		35					40					45							
Asn	Phe	Phe	Asp	Gly	Lys	Leu	Leu	Lys	Glu	Ala	Leu	Gly	Lys	Ala	Leu				
	50					55					60								
Val	Pro	Phe	Tyr	Pro	Met	Ala	Gly	Arg	Leu	Lys	Arg	Asp	Glu	Asp	Gly				
	65				70					75					80				
Arg	Ile	Glu	Ile	Asp	Cys	Asn	Ala	Glu	Gly	Val	Leu	Phe	Val	Glu	Ala				
			85						90					95					
Glu	Thr	Pro	Ser	Val	Ile	Asp	Asp	Phe	Gly	Asp	Phe	Ala	Pro	Thr	Leu				
		100					105						110						
Glu	Leu	Lys	Gln	Leu	Ile	Pro	Thr	Val	Asp	Tyr	Ser	Gly	Gly	Ile	Ser				
		115					120					125							
Thr	Tyr	Pro	Leu	Leu	Ala	Leu	Gln	Val	Thr	His	Phe	Lys	Cys	Gly	Gly				
	130					135					140								
Val	Ser	Leu	Gly	Val	Gly	Met	Gln	His	His	Ala	Ala	Asp	Gly	Phe	Ser				
145					150					155					160				

Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp
 165 170 175
 Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp
 180 185 190
 Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro
 195 200 205
 Ser Leu Lys Thr Pro Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser
 210 215 220
 Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala
 225 230 235 240
 Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala
 245 250 255
 Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp
 260 265 270
 Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile
 275 280 285
 Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr
 290 295 300
 Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala
 305 310 315 320
 Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu
 325 330 335
 Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu
 340 345 350
 Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser
 355 360 365
 Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro
 370 375 380
 Thr Phe Met Gly Pro Gly Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val
 385 390 395 400
 Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu
 405 410 415
 Gln Ser Glu His Met Lys Leu Phe Gln Lys Phe Phe Tyr Asp Ile
 420 425 430

<210> 23
 <211> 426
 <212> PRT
 <213> Citrus limon
 <223> Lemon acyl transferase

<400> 23
 Met Asp Leu Gln Ile Thr Cys Thr Glu Ile Ile Lys Pro Ser Ser Pro
 1 5 10 15

Thr Pro Gln His Gln Ser Thr Tyr Lys Leu Ser Ile Ile Asp Gln Leu

20					25					30					
Thr	Pro	Asn	Val	Tyr	Phe	Ser	Ile	Ile	Leu	Leu	Tyr	Ser	Lys	Ala	Gly
		35					40					45			
Glu	Ser	Thr	Ala	Lys	Thr	Ser	Asp	His	Leu	Lys	Glu	Ser	Leu	Ser	Asn
	50					55					60				
Thr	Leu	Thr	His	Tyr	Tyr	Pro	Leu	Ala	Gly	Gln	Leu	Lys	Tyr	Asp	Gln
	65					70					75				80
Leu	Ile	Val	Asp	Cys	Asn	Asp	Gln	Gly	Val	Pro	Phe	Ile	Glu	Ala	His
				85					90					95	
Val	Thr	Asn	Asp	Met	Arg	Gln	Leu	Leu	Lys	Ile	Pro	Asn	Ile	Asp	Val
			100					105					110		
Leu	Glu	Gln	Leu	Leu	Pro	Phe	Lys	Pro	His	Glu	Gly	Phe	Asp	Ser	Asp
		115					120						125		
Arg	Ser	Asn	Leu	Thr	Val	Gln	Val	Asn	Tyr	Phe	Gly	Cys	Glu	Gly	Met
	130					135					140				
Ala	Ile	Gly	Leu	Cys	Phe	Arg	His	Lys	Val	Ile	Asp	Ala	Thr	Thr	Ala
	145					150					155				160
Ala	Phe	Phe	Val	Lys	Asn	Trp	Gly	Val	Ile	Ala	Arg	Gly	Ala	Gly	Glu
				165					170					175	
Ile	Lys	Asp	Val	Ile	Ile	Asp	His	Ala	Ser	Leu	Phe	Pro	Ala	Arg	Asp
			180					185					190		
Leu	Ser	Cys	Leu	Thr	Lys	Ser	Val	Asp	Glu	Glu	Phe	Leu	Lys	Pro	Glu
		195					200					205			
Ser	Glu	Thr	Lys	Arg	Phe	Val	Phe	Asp	Gly	Ala	Thr	Ile	Ala	Ser	Leu
	210					215					220				
Gln	Glu	Thr	Phe	Ala	Ser	Phe	Glu	Arg	Arg	Pro	Thr	Arg	Phe	Glu	Val
	225					230					235				240
Val	Ser	Ala	Val	Ile	Leu	Gly	Ala	Leu	Ile	Thr	Ala	Thr	Arg	Glu	Ser
				245					250					255	
Asp	Asp	Glu	Ser	Asn	Val	Pro	Glu	Arg	Leu	Asp	Thr	Ile	Ile	Ser	Val
			260					265					270		
Asn	Leu	Arg	Gln	Arg	Met	Asn	Pro	Pro	Phe	Pro	Glu	His	Cys	Met	Gly
		275					280					285			
Asn	Ile	Ile	Ser	Gly	Gly	Leu	Val	Tyr	Trp	Pro	Leu	Glu	Lys	Lys	Val
	290					295					300				
Asp	Tyr	Gly	Cys	Leu	Ala	Lys	Glu	Ile	His	Glu	Ser	Ile	Lys	Lys	Val
	305					310					315				320
Asp	Asp	Gln	Phe	Ala	Arg	Lys	Phe	Tyr	Gly	Asp	Ala	Glu	Phe	Leu	Asn
				325					330					335	
Leu	Pro	Arg	Leu	Ala	Gly	Ala	Glu	Asp	Val	Lys	Lys	Arg	Glu	Phe	Trp
			340					345					350		

Val Thr Ser Trp Cys Lys Thr Pro Leu Tyr Glu Ala Asp Phe Gly Trp
355 360 365

Gly Asn Pro Lys Trp Ala Gly Asn Ser Met Arg Leu Asn Gln Ile Thr
370 375 380

Val Phe Phe Asp Ser Ser Asp Gly Glu Gly Val Glu Ala Trp Val Gly
385 390 395 400

Leu Pro Arg Lys Asp Met Ala Arg Phe Glu Lys Asp Ser Gly Ile Leu
405 410 415

Ala Tyr Thr Ser Pro Asn Pro Ser Ile Phe
420 425

<210> 24
<211> 491
<212> PRT
<213> Citrus limon
<223> Lemon acyl transferase

<400> 24
Met Ala Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr
1 5 10 15

Lys Val Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr
20 25 30

Leu Asp Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val
35 40 45

Glu Arg Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe
50 55 60

Asn Ser Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu
65 70 75 80

Leu His Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala
85 90 95

Ala Lys Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser
100 105 110

Phe Ala Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His
115 120 125

Leu Ser Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val
130 135 140

Pro Gln Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln
145 150 155 160

Ile Thr Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His
165 170 175

His Ala Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp
180 185 190

Ala Tyr Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser
195 200 205

Pro Glu Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr

210					215					220					
Gly	Gln	Asp	Met	Leu	Gln	Leu	Asn	Lys	Trp	Val	Val	Gly	Ser	Asp	Asn
225					230					235					240
Ser	Asp	Pro	Gln	Lys	Ile	Arg	Ser	Leu	Lys	Val	Leu	Pro	Phe	Leu	Asp
				245					250					255	
Ser	Glu	Ser	Leu	Asn	Lys	Leu	Val	Arg	Ala	Thr	Phe	Glu	Leu	Thr	Arg
			260					265					270		
Glu	Asp	Ile	Thr	Lys	Leu	Arg	His	Lys	Val	Asn	His	Gln	Leu	Ser	Lys
		275					280					285			
Ser	Ser	Lys	Ser	Lys	Gln	Val	Arg	Leu	Ser	Thr	Phe	Val	Leu	Thr	Leu
	290					295					300				
Ala	Tyr	Val	Phe	Val	Cys	Met	Ala	Lys	Ala	Lys	Leu	Ala	Lys	Ala	Lys
305					310					315					320
Thr	Glu	Ala	Glu	Ala	Ala	Ala	Gly	Asn	Asp	Glu	Ile	Lys	Asn	Ile	Ile
				325					330					335	
Val	Gly	Phe	Thr	Ala	Asp	Tyr	Arg	Ser	Arg	Leu	Asp	Pro	Pro	Ile	Pro
			340					345					350		
Leu	Asn	Tyr	Phe	Gly	Asn	Cys	Asn	Gly	Arg	His	Cys	Glu	Thr	Ala	Lys
	355						360					365			
Ala	Ser	Asp	Phe	Val	Gln	Glu	Asn	Gly	Val	Ala	Phe	Val	Ala	Glu	Met
	370					375					380				
Leu	Ser	Asp	Met	Val	Lys	Gly	Ile	Asp	Ala	Asp	Ala	Ile	Glu	Ala	Asn
385					390					395					400
Asp	Asp	Lys	Val	Ser	Glu	Ile	Leu	Glu	Ile	Leu	Lys	Glu	Gly	Ala	Met
			405						410					415	
Ile	Phe	Ser	Val	Ala	Gly	Ser	Thr	Gln	Phe	Asp	Val	Tyr	Gly	Ser	Asp
			420					425					430		
Phe	Gly	Trp	Gly	Arg	Pro	Lys	Lys	Val	Glu	Ile	Val	Ser	Ile	Asp	Arg
		435					440					445			
Thr	Gln	Ala	Ile	Ser	Leu	Ala	Glu	Arg	Arg	Asp	Gly	Gly	Gly	Gly	Val
	450					455					460				
Glu	Val	Gly	Val	Val	Leu	Glu	Lys	Gln	Gln	Met	Glu	Val	Phe	Glu	Ser
465					470					475					480
Val	Phe	Ala	Asp	Gly	Leu	Lys	Asn	Asp	Leu	Val					
				485					490						

<210> 25
 <211> 447
 <212> PRT
 <213> Citrus limon
 <223> Lemon acyl transferase

<400> 25
 Met Ala Ala Ser Ser Leu His Gly Lys Glu Ala Thr Val Ile Tyr Pro
 1 5 10 15

Ser Glu Pro Thr 20 Pro Ser Thr Val 25 Leu Ser Leu Ser Ala Leu Asp Ser 30
 Gln Leu Phe 35 Leu Arg Phe Thr 40 Ile Glu Tyr Leu Leu Val 45 Tyr Arg Pro
 Arg Pro 50 Gly Leu Asp Pro 55 Ala Thr Val Ala Arg Val 60 Lys Ser Ala
 Leu Ala Lys Ala Leu 70 Val Pro Tyr Tyr Pro 75 Leu Ala Gly Arg Val Arg 80
 Ala Lys Gln Asp Gly 85 Ser Gly Leu Leu Glu 90 Val Val Cys Leu Gly Gln 95
 Gly Ala Val 100 Phe Ile Glu Ala Val 105 Asp Arg Glu Ser Thr 110 Ile Thr Asp
 Phe Glu Ser 115 Ala Pro Arg Tyr Val 120 Thr Gln Trp Arg Lys Leu Leu Ser 125
 Leu Tyr Val Ala Asp Val 130 Leu Lys Gly Ala Pro 140 Pro Leu Val Val Gln
 Leu Thr Trp Leu Arg Asp 150 Gly Ala Ala Ala Leu Gly Ile Gly Phe Asn 160
 His Cys Val Cys Asp 165 Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu Phe 175
 Thr Glu Leu Cys Thr Ser Arg His 180 Asn Glu Leu Gly Gly Gly His Ser 190
 Leu Pro Lys Pro Val Trp Asp Arg 200 His Leu Met Asn Ser Ser Ser Ser 205
 Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu Glu 220
 Phe Asn Arg Val Ala Asp 230 Leu Cys Gly Phe Val Ser Arg Phe Ser Asn 240
 Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu Asn 255
 Glu Leu Arg Lys 260 Leu Ala Leu Ser Thr 265 Ser Arg Pro Ser Glu Leu Ala 270
 Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp Ala 285
 Arg Ser Leu Asn Leu Pro Ser 295 Asn Gln Ile Leu Lys Leu Leu Phe Ser 300
 Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr Tyr 320
 Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp Leu 335
 Thr Glu Lys Asp 340 Leu Gly His Ala Ala Met Leu Val Lys Lys Ala Lys 350

Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val Ser
 355 360 365
 His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser Gln
 370 375 380
 Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg Pro
 385 390 395 400
 Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu Pro
 405 410 415
 Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro Thr
 420 425 430
 Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp
 435 440 445

<210> 26
 <211> 456
 <212> PRT
 <213> Cucumis melo
 <223> Honey dew melon alcohol acyl transferase

<400> 26
 Met Asp Phe Ser Phe His Val Arg Lys Cys Gln Pro Glu Leu Ile Ala
 1 5 10 15
 Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp
 20 25 30
 Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro
 35 40 45
 His Asn Pro Ser Leu Glu Gly Arg Asp Pro Val Lys Val Ile Lys Glu
 50 55 60
 Ala Ile Gly Lys Ala Leu Val Phe Tyr Tyr Pro Leu Ala Gly Arg Leu
 65 70 75 80
 Arg Glu Gly Pro Gly Arg Lys Leu Phe Val Glu Cys Thr Gly Glu Gly
 85 90 95
 Ile Leu Phe Ile Glu Ala Asp Ala Asp Val Ser Leu Glu Glu Phe Trp
 100 105 110
 Asp Thr Leu Pro Tyr Ser Leu Ser Ser Met Gln Asn Asn Ile Ile His
 115 120 125
 Asn Ala Leu Asn Ser Asp Glu Val Leu Asn Ser Pro Leu Leu Leu Ile
 130 135 140
 Gln Val Thr Arg Leu Lys Cys Gly Gly Phe Ile Phe Gly Leu Cys Phe
 145 150 155 160
 Asn His Thr Met Ala Asp Gly Phe Gly Ile Val Gln Phe Met Lys Ala
 165 170 175
 Thr Ala Glu Ile Ala Arg Gly Ala Phe Ala Pro Ser Ile Leu Pro Val
 180 185 190
 Trp Gln Arg Ala Leu Leu Thr Ala Arg Asp Pro Pro Arg Ile Thr Phe

195					200					205					
Arg	His	Tyr	Glu	Tyr	Asp	Gln	Val	Val	Asp	Met	Lys	Ser	Gly	Leu	Ile
210						215					220				
Pro	Val	Asn	Ser	Lys	Ile	Asp	Gln	Leu	Phe	Phe	Phe	Ser	Gln	Leu	Gln
225					230					235					240
Ile	Ser	Thr	Leu	Arg	Gln	Thr	Leu	Pro	Ala	His	Leu	His	Asp	Cys	Pro
				245					250					255	
Ser	Phe	Glu	Val	Leu	Thr	Ala	Tyr	Val	Trp	Arg	Leu	Arg	Thr	Ile	Ala
			260					265					270		
Leu	Gln	Phe	Lys	Pro	Glu	Glu	Glu	Val	Arg	Phe	Leu	Cys	Val	Met	Asn
		275					280					285			
Leu	Arg	Ser	Lys	Ile	Asp	Ile	Pro	Leu	Gly	Tyr	Tyr	Gly	Asn	Ala	Val
	290					295					300				
Val	Val	Pro	Ala	Val	Ile	Thr	Thr	Ala	Ala	Lys	Leu	Cys	Gly	Asn	Pro
305					310					315					320
Leu	Gly	Tyr	Ala	Val	Asp	Leu	Ile	Arg	Lys	Ala	Lys	Ala	Lys	Ala	Thr
				325					330					335	
Met	Glu	Tyr	Ile	Lys	Ser	Thr	Val	Asp	Leu	Met	Val	Ile	Lys	Gly	Arg
			340					345					350		
Pro	Tyr	Phe	Thr	Val	Val	Gly	Ser	Phe	Met	Met	Ser	Asp	Leu	Thr	Arg
		355					360					365			
Ile	Gly	Val	Glu	Asn	Val	Asp	Phe	Gly	Trp	Gly	Lys	Ala	Ile	Phe	Gly
	370					375					380				
Gly	Pro	Thr	Thr	Thr	Gly	Ala	Arg	Ile	Thr	Arg	Gly	Leu	Val	Ser	Phe
385					390					395					400
Cys	Val	Pro	Phe	Met	Asn	Arg	Asn	Gly	Glu	Lys	Gly	Thr	Ala	Leu	Ser
				405					410					415	
Leu	Cys	Leu	Pro	Pro	Pro	Ala	Met	Glu	Arg	Phe	Arg	Ala	Asn	Val	His
			420					425					430		
Ala	Ser	Leu	Gln	Val	Lys	Gln	Val	Val	Asp	Ala	Val	Asp	Ser	His	Met
		435					440					445			
Gln	Thr	Ile	Gln	Ser	Ala	Ser	Lys								
	450					455									
<210> 27															
<211> 397															
<212> PRT															
<213> Fragaria x ananassa															
<223> Strawberry aminotransferase															
<400> 27															
Met	Ala	Lys	Leu	Gln	Ala	Gly	Tyr	Leu	Phe	Pro	Glu	Ile	Ala	Arg	Arg
1				5					10					15	
Arg	Asn	Ala	His	Leu	Gln	Lys	His	Pro	Asp	Ala	Lys	Ile	Ile	Pro	Leu
			20					25					30		

Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu Tyr Ile Thr Ser Ala
 35 40 45
 Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu Glu Gly Tyr Ser Gly
 50 55 60
 Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg Val Ala Ile Ala Lys
 65 70 75 80
 Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp Asp Ile Phe Val Ser
 85 90 95
 Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln Val Leu Phe Gly Ala
 100 105 110
 Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr Pro Ala Tyr Val Asp
 115 120 125
 Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr Gln Lys Ser Val Gln
 130 135 140
 Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr Pro Asp Asn Gly Phe
 145 150 155 160
 Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp Ile Ile Phe Phe Cys
 165 170 175
 Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr Arg Glu Gln Leu Thr
 180 185 190
 Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser Ile Ile Val Tyr Asp
 195 200 205
 Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn Pro Arg Ser Ile Phe
 210 215 220
 Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu Thr Ser Ser Phe Ser
 225 230 235 240
 Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly Trp Thr Val Val Pro
 245 250 255
 Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val Ala Lys Asp Phe Asn
 260 265 270
 Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser Thr Ile Ile Gln Ala
 275 280 285
 Gly Gly Leu Ala Cys Leu Gln Pro Lys Gly Val Lys Ala Met His Gly
 290 295 300
 Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile Ile Met Glu Thr Phe
 305 310 315 320
 Asn Ser Leu Gly Phe Asn Val Tyr Gly Gly Thr Asn Ala Pro Tyr Val
 325 330 335
 Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp Val Phe Ala Glu Ile
 340 345 350
 Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe Gly Pro
 355 360 365

Gly Gly Glu Gly Phe Ile Arg Val Ser Ala Phe Gly His Arg Lys Asn
 370 375 380

Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu Tyr Lys
 385 390 395

<210> 28

<211> 458

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry thiolase

<400> 28

Met Glu Lys Ala Ile Asn Arg Gln Lys Val Leu Leu Asp His Leu Arg
 1 5 10 15

Pro Ser Ser Ser Ser Asp Asp Ser Ser Leu Ser Ala Ser Val Cys Ala
 20 25 30

Ala Gly Asp Ser Ala Ala Tyr Ala Arg Asn His Val Phe Gly Asp Asp
 35 40 45

Val Val Ile Val Ala Ala Phe Arg Thr Pro Leu Cys Lys Ala Lys Arg
 50 55 60

Gly Gly Phe Lys Tyr Thr Tyr Ala Asp Asp Leu Leu Ala Pro Val Leu
 65 70 75 80

Lys Ala Val Val Glu Lys Thr Asn Leu Asn Pro Lys Glu Val Gly Asp
 85 90 95

Ile Val Val Gly Thr Val Leu Ala Pro Gly Ser Gln Arg Ala Ser Glu
 100 105 110

Cys Arg Met Ala Ala Phe Tyr Ala Gly Phe Pro Glu Thr Val Pro Val
 115 120 125

Arg Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln Ala Val Ala Asp
 130 135 140

Val Ala Ala Ala Ile Arg Ala Gly Phe Tyr Asp Ile Gly Ile Gly Ala
 145 150 155 160

Gly Leu Glu Ser Met Thr Ala Asn Pro Met Ala Trp Glu Gly Asp Val
 165 170 175

Asn Pro Lys Val Lys Ile Phe Glu Gln Ala Gln Asn Cys Leu Leu Pro
 180 185 190

Met Gly Val Thr Ser Glu Asn Val Ala His Arg Phe Gly Val Ser Arg
 195 200 205

Gln Glu Gln Asp Gln Ala Ala Val Asp Ser His Arg Lys Ala Ala Ala
 210 215 220

Ala Ala Ala Ala Gly Arg Phe Lys Asp Glu Ile Ile Pro Val Ala Thr
 225 230 235 240

Lys Ile Val Asp Pro Lys Ser Gly Asp Glu Lys Pro Val Thr Ile Ser
 245 250 255

Val Asp Asp Gly Ile Arg Asn Thr Thr Leu Ala Asp Leu Ala Lys Leu

260					265					270					
Lys	Pro	Val	Phe	Lys	Lys	Asp	Gly	Thr	Thr	Thr	Ala	Gly	Asn	Ser	Ser
		275					280					285			
Gln	Val	Ser	Asp	Gly	Ala	Gly	Ala	Val	Leu	Leu	Met	Lys	Arg	Ser	Val
		290				295					300				
Ala	Asp	Gln	Lys	Gly	Leu	Pro	Ile	Leu	Gly	Val	Phe	Arg	Asn	Phe	Val
305					310					315					320
Ala	Val	Gly	Val	Asp	Pro	Ala	Ile	Met	Gly	Val	Gly	Pro	Ala	Ala	Ala
				325					330					335	
Ile	Pro	Val	Ala	Val	Lys	Ala	Ala	Gly	Leu	Glu	Leu	Asp	Asp	Ile	Asp
			340					345					350		
Leu	Phe	Glu	Ile	Asn	Glu	Ala	Phe	Ala	Ser	Gln	Phe	Val	Tyr	Cys	Arg
		355					360					365			
Asn	Lys	Leu	Gly	Leu	Asp	Pro	Glu	Lys	Ile	Asn	Val	Asn	Gly	Gly	Ala
		370				375					380				
Met	Ala	Ile	Gly	His	Pro	Leu	Gly	Ala	Thr	Gly	Ala	Arg	Cys	Val	Ala
385					390					395					400
Thr	Leu	Leu	His	Glu	Met	Lys	Arg	Arg	Gly	Lys	Asp	Cys	Arg	Tyr	Gly
				405					410					415	
Val	Ile	Ser	Met	Cys	Ile	Gly	Thr	Gly	Met	Gly	Ala	Ala	Ala	Val	Phe
			420					425					430		
Glu	Arg	Gly	Asp	Arg	Thr	Asp	Glu	Leu	Cys	Asn	Ala	Arg	Lys	Val	Glu
		435				440					445				
Ser	Leu	Asn	Phe	Leu	Ser	Lys	Asp	Val	Arg						
		450				455									

<210> 29
 <211> 605
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry pyruvate decarboxylase

<400> 29
 Met Asp Thr Lys Ile Gly Ser Ile Asp Val Cys Lys Thr Glu Asn His
 1 5 10 15
 Asp Val Gly Cys Leu Pro Asn Ser Ala Thr Ser Thr Val Gln Asn Ser
 20 25 30
 Val Pro Ser Thr Ser Leu Ser Ser Ala Asp Ala Thr Leu Gly Arg His
 35 40 45
 Leu Ala Arg Arg Leu Val Gln Ile Gly Val Thr Asp Val Phe Thr Val
 50 55 60
 Pro Gly Asp Phe Asn Leu Thr Leu Leu Asp His Leu Ile Ala Glu Pro
 65 70 75 80
 Gly Leu Thr Asn Ile Gly Cys Cys Asn Glu Leu Asn Ala Gly Tyr Ala
 85 90 95

Ala Asp Gly Tyr Ala Arg Ser Arg Gly Val Gly Ala Cys Val Val Thr
 100 105 110
 Phe Thr Val Gly Gly Leu Ser Val Leu Asn Ala Ile Ala Gly Ala Tyr
 115 120 125
 Ser Glu Asn Leu Pro Val Ile Cys Ile Val Gly Gly Pro Asn Ser Asn
 130 135 140
 Asp Tyr Gly Thr Asn Arg Ile Leu His His Thr Ile Gly Leu Pro Asp
 145 150 155 160
 Phe Ser Gln Glu Leu Arg Cys Phe Gln Thr Val Thr Cys Phe Gln Ala
 165 170 175
 Val Val Asn Asn Leu Glu Asp Ala His Glu Met Ile Asp Thr Ala Ile
 180 185 190
 Ser Thr Ala Leu Lys Glu Ser Lys Pro Val Tyr Ile Ser Ile Gly Cys
 195 200 205
 Asn Leu Ala Gly Ile Pro His Pro Thr Phe Ser Arg Glu Pro Val Pro
 210 215 220
 Phe Ser Leu Ser Pro Lys Leu Ser Asn Lys Trp Gly Leu Glu Ala Ala
 225 230 235 240
 Val Glu Ala Ala Ala Glu Phe Leu Asn Lys Ala Val Lys Pro Val Met
 245 250 255
 Val Gly Gly Pro Lys Leu Arg Ser Ala His Ala Gly Asp Ala Phe Val
 260 265 270
 Glu Leu Ala Asp Ala Ser Gly Phe Ala Leu Ala Val Met Pro Ser Ala
 275 280 285
 Lys Gly Gln Val Pro Glu His His Pro His Phe Ile Gly Thr Tyr Trp
 290 295 300
 Gly Ala Val Ser Thr Ala Phe Cys Ala Glu Ile Val Glu Ser Ala Asp
 305 310 315 320
 Ala Tyr Leu Phe Ala Gly Pro Ile Phe Asn Asp Tyr Ser Ser Val Gly
 325 330 335
 Tyr Ser Leu Leu Leu Lys Lys Glu Lys Ala Ile Ile Val Gln Pro Asp
 340 345 350
 Arg Val Thr Ile Gly Asn Gly Pro Thr Phe Gly Cys Val Leu Met Lys
 355 360 365
 Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys His Asn Asn Thr Ala
 370 375 380
 His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp Gly His Pro Leu Lys
 385 390 395 400
 Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val Leu Phe Lys His Ile
 405 410 415
 Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile Ala Glu Thr Gly Asp
 420 425 430

Ser Trp Phe Asn Cys Gln Lys Leu Lys Leu Pro Pro Gly Cys Gly Tyr
 435 440 445
 Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp Ser Val Gly Ala Thr
 450 455 460
 Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg Val Ile Ser Phe Ile
 465 470 475 480
 Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp Val Ser Thr Met Ile
 485 490 495
 Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile Asn Asn Gly Gly Tyr
 500 505 510
 Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr Asn Val Ile Lys Asn
 515 520 525
 Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His Asn Gly Glu Gly Lys
 530 535 540
 Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu Leu Ile Glu Ala Ile
 545 550 555 560
 Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe Cys Phe Ile Glu Val
 565 570 575
 Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu Leu Glu Trp Gly Ser
 580 585 590
 Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn Pro Gln
 595 600 605

<210> 30
 <211> 333
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry alcohol dehydrogenase

<400> 30
 Met Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp
 1 5 10 15
 Ala Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Phe Ser Arg
 20 25 30
 Arg Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly
 35 40 45
 Ile Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser
 50 55 60
 Thr Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu
 65 70 75 80
 Val Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val
 85 90 95

Gly Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His
 100 105 110
 Leu Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr
 115 120 125
 Tyr Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala
 130 135 140
 Asp Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly
 145 150 155 160
 Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg
 165 170 175
 Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu
 180 185 190
 Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val
 195 200 205
 Lys Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Arg
 210 215 220
 Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln
 225 230 235 240
 Met Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser
 245 250 255
 Ala Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly
 260 265 270
 Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val
 275 280 285
 Phe Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly
 290 295 300
 Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Lys His Asn
 305 310 315 320
 Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
 325 330

<210> 31
 <211> 326
 <212> PRT
 <213> *Fragaria x ananassa*
 <223> Strawberry alcohol dehydrogenase

<400> 31
 Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val
 1 5 10 15
 Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr
 20 25 30
 Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val
 35 40 45
 Gly Cys Lys Val Lys Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp

50					55					60					
Leu	His	Gly	Arg	Leu	Arg	Pro	Thr	Cys	Glu	Asn	Cys	Ile	His	His	Leu
65					70					75					80
Glu	Asn	Tyr	Cys	Pro	Asn	Leu	Ile	Gln	Thr	Tyr	Gly	Ser	Lys	Tyr	Tyr
				85					90					95	
Asp	Gly	Thr	Met	Thr	Tyr	Gly	Gly	Tyr	Ser	Asn	Asn	Met	Val	Thr	Asp
			100					105					110		
Glu	His	Phe	Ile	Val	Arg	Ile	Pro	Asp	Asn	Leu	Pro	Leu	Asp	Gly	Ala
		115					120					125			
Ala	Pro	Leu	Leu	Cys	Ala	Gly	Ile	Thr	Thr	Tyr	Ser	Pro	Trp	Arg	Tyr
	130					135					140				
Tyr	Gly	Leu	Asp	Lys	Pro	Gly	Met	His	Leu	Gly	Val	Glu	Trp	Pro	Arg
145					150					155					160
Arg	Phe	Arg	Ser	Arg	Pro	Pro	Leu	Asn	Leu	Pro	Gly	Leu	Trp	Gly	Ser
				165					170					175	
Arg	Leu	Gln	Ser	Leu	Val	Pro	Pro	Leu	Ile	Lys	Glu	Gly	Gly	Ser	Tyr
			180					185					190		
Gly	Thr	Ser	Pro	Ala	Leu	Met	His	Ser	Leu	Leu	Arg	Thr	Asp	Gln	Asp
		195					200					205			
Gln	Met	Glu	Ala	Ala	Met	Ser	Thr	Met	Asp	Gly	Ile	Ile	Asp	Thr	Val
	210					215					220				
Pro	Ala	Val	Arg	Pro	Leu	Glu	Pro	Leu	Ile	Ser	Leu	Leu	Lys	Thr	Asn
225					230					235					240
Gly	Lys	Val	Val	Thr	Val	Gly	Ile	Ala	Val	Gln	Pro	Leu	Asp	Leu	Pro
				245					250					255	
Val	Phe	Pro	Leu	Ile	Ile	Gly	Arg	Lys	Met	Val	Ala	Gly	Ser	Ala	Ile
			260					265					270		
Gly	Gly	Met	Lys	Glu	Thr	Gln	Glu	Met	Ile	Asp	Phe	Ala	Ala	Glu	His
		275					280					285			
Asn	Ile	Thr	Ala	Asp	Ile	Glu	Val	Ile	Pro	Ile	Asp	Tyr	Leu	Asn	Thr
		290				295					300				
Ala	Met	Glu	Arg	Val	Val	Lys	Lys	Asp	Val	Arg	Phe	Arg	Phe	Val	Ile
305					310					315					320
Asp	Val	Glu	Asn	Thr	Leu										
				325											

<210> 32
 <211> 278
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry alcohol dehydrogenase

<400> 32
 Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys Leu
 1 5 10 15

Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu Asn
 20 25 30
 Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp Gly
 35 40 45
 Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp Glu Ala
 50 55 60
 Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala Pro
 65 70 75 80
 Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe Gly
 85 90 95
 Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly Leu
 100 105 110
 Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val Thr
 115 120 125
 Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His Leu
 130 135 140
 Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln Ala
 145 150 155 160
 Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val His
 165 170 175
 Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu Val
 180 185 190
 Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser Leu
 195 200 205
 Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile Lys
 210 215 220
 Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr Ala
 225 230 235 240
 Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu Arg
 245 250 255
 Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly Asn
 260 265 270
 Thr Leu Lys Pro Ala Ile
 275

<210> 33
 <211> 283
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry alcohol dehydrogenase

<400> 33
 Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg
 1 5 10 15

Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile

20					25					30					
Cys	His	Ser	Asp	Leu	His	Met	Val	Lys	Asn	Glu	Trp	Gly	Phe	Ser	Thr
		35					40					45			
Tyr	Pro	Leu	Val	Pro	Gly	His	Glu	Ile	Val	Gly	Glu	Val	Thr	Glu	Val
	50					55					60				
Gly	Ser	Lys	Val	Gln	Lys	Phe	Lys	Val	Gly	Asp	Arg	Val	Gly	Val	Gly
	65					70					75				80
Cys	Val	Val	Gly	Ser	Cys	Arg	Ser	Cys	Glu	Asn	Cys	Thr	Asp	His	Leu
				85					90					95	
Glu	Asn	Tyr	Cys	Pro	Lys	Gln	Ile	Leu	Thr	Tyr	Gly	Ala	Lys	Tyr	Tyr
			100					105					110		
Asp	Gly	Thr	Thr	Thr	Tyr	Gly	Gly	Tyr	Ser	Asp	Ile	Met	Val	Ala	Asp
		115					120					125			
Glu	His	Phe	Ile	Val	Arg	Ile	Pro	Asp	Asn	Leu	Pro	Leu	Asp	Gly	Ala
	130					135					140				
Ala	Pro	Leu	Leu	Cys	Ala	Gly	Ile	Thr	Thr	Tyr	Ser	Pro	Leu	Arg	Tyr
	145					150					155				160
Phe	Gly	Leu	Asp	Lys	Pro	Gly	Met	His	Val	Gly	Val	Val	Gly	Leu	Gly
				165					170					175	
Gly	Leu	Gly	His	Val	Ala	Val	Lys	Phe	Ala	Lys	Ala	Met	Gly	Val	Lys
			180					185					190		
Val	Thr	Val	Ile	Ser	Thr	Ser	Pro	Lys	Lys	Glu	Glu	Glu	Ala	Leu	Lys
		195					200					205			
His	Leu	Gly	Ala	Asp	Ser	Phe	Phe	Val	Ser	Arg	Asp	Gln	Asp	Gln	Met
	210					215					220				
Gln	Ala	Ala	Ile	Gly	Thr	Met	Asp	Gly	Ile	Ile	Asp	Thr	Val	Ser	Ala
	225					230					235				240
Gln	His	Pro	Leu	Leu	Pro	Leu	Ile	Gly	Leu	Leu	Lys	Ser	His	Gly	Lys
				245					250					255	
Leu	Val	Met	Val	Gly	Ala	Pro	Glu	Lys	Pro	Leu	Glu	Leu	Pro	Val	Phe
			260					265					270		
Pro	Leu	Leu	Met	Gly	Arg	Lys	Met	Gly	Ser	Trp					
			275				280								

<210> 34
 <211> 188
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry alcohol dehydrogenase

<400> 34
 Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val
 1 5 10 15
 Val Gly Leu Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala
 20 25 30

Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp
 35 40 45
 Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp
 50 55 60
 Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp
 65 70 75 80
 Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys
 85 90 95
 Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu
 100 105 110
 Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser
 115 120 125
 Asn Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala
 130 135 140
 Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
 145 150 155 160
 Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe
 165 170 175
 Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr
 180 185

<210> 35
 <211> 1227
 <212> DNA
 <213> Fragaria x ananassa

<220>
 <221> CDS
 <222> (2)..(979)
 <223> partial cDNA

<220>
 <223> Strawberry alcohol dehydrogenase

<400> 35
 g gaa aca gga gca acg gac gta aga ttc aaa gtg ttg tac tgt gga gta 49
 Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val
 1 5 10 15
 tgc cat tcg gac ata cac atg gcc aaa aat gat tgg ggg act tct acc 97
 Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr
 20 25 30
 tat cct att gta cct ggg cat gaa ctt gtt ggt gta gta aca gaa gta 145
 Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val
 35 40 45
 gga tgc aaa gta aag aaa ttc aaa agt tgg aga caa ggt cgg tgt tgg 193
 Gly Cys Lys Val Lys Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp
 50 55 60
 ttg cat ggt cga ctc aga cca act tgc gaa aat tgt atc cat cac cta 241
 Leu His Gly Arg Leu Arg Pro Thr Cys Glu Asn Cys Ile His His Leu

65	70	75	80	
gaa aat tac tgt ccg aat ctg ata caa acc tac ggt tct aaa tac tac	Pro Asn Leu Ile Gln Thr Tyr Ser Lys Tyr Tyr	289		
Glu Asn Tyr Cys	85	90	95	
gac gga acc atg aca tac gga ggt tac tcg aac aac atg gtg act gat	Asp Gly Thr Met Thr Tyr Gly Gly Tyr Ser Asn Asn Met Val Thr Asp	337		
	100	105	110	
gag cac ttc att gtt cgg atc ccg gac aac tta cct ctt gat ggc gct	Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala	385		
	115	120	125	
gct ccg ctt cta tgt gcc ggg att aca act tac agc cca tgg aga tat	Ala Pro Leu Leu Cys Ala Ile Thr Thr Tyr Ser Pro Trp Arg Tyr	433		
	130	135	140	
tat gga ctt gac aaa ccc ggt atg cat ctt ggt gtt gaa tgg cct agg	Tyr Gly Leu Asp Lys Pro Gly Met His Leu Gly Val Glu Trp Pro Arg	481		
	145	150	155	160
cgg ttt agg tca cgt ccg ccg tta aat ttg cca ggg ctt tgg ggc tca	Arg Phe Arg Ser Arg Pro Pro Leu Asn Leu Pro Gly Leu Trp Gly Ser	529		
	165	170	175	
agg tta cag tca tta gta cct ccc cta att aaa gaa gga ggc agc tat	Arg Leu Gln Ser Leu Val Pro Pro Leu Ile Lys Glu Gly Gly Ser Tyr	577		
	180	185	190	
gga aca tct ccc gcg ctg atg cat tcc ctg ctt aga act gac caa gat	Gly Thr Ser Pro Ala Leu Met His Ser Leu Leu Arg Thr Asp Gln Asp	625		
	195	200	205	
cag atg gag gct gcc atg agc aca atg gat ggt atc att gac aca gtt	Gln Met Glu Ala Ala Met Ser Thr Met Asp Gly Ile Ile Asp Thr Val	673		
	210	215	220	
cct gca gtt cga cct cta gag cct ttg att tca ttg ttg aag act aat	Pro Ala Val Arg Pro Leu Glu Pro Leu Ile Ser Leu Leu Lys Thr Asn	721		
	225	230	235	240
gga aaa gtt gtt acc gtt ggt ata gca gtg cag cca ctc gat ctc cca	Gly Lys Val Val Thr Val Gly Ile Ala Val Gln Pro Leu Asp Leu Pro	769		
	245	250	255	
gtt ttc cct ttg ata ata gga agg aag atg gta gct ggt agt gcc att	Val Phe Pro Leu Ile Ile Gly Arg Lys Met Val Ala Gly Ser Ala Ile	817		
	260	265	270	
gga ggt atg aaa gag acg caa gag atg att gat ttt gct gct gaa cat	Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His	865		
	275	280	285	
aac ata aca gct gac atc gag gtc atc ccg att gat tac ctg aac acc	Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr	913		
	290	295	300	
gca atg gaa cgc gtt gtc aaa aaa gat gtc agg ttt cga ttt gtc atc	Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile	961		
	305	310	315	320

gac gtt gag aac aca ttg taagtccgcc taagtttttc attcaattct 1009
 Asp Val Glu Asn Thr Leu
 325

gttaataaga ctatgcatta atatatgact gactctccat aggatggagt tatcagtctt 1069

caaattttcta gacatatttt gtgatcaaat aaatggaatg gctttgtttt ccttttccac 1129

taagattaga tttcagttgt attgttttta aagagattga tgtttttatt aattgtaaca 1189

gtgttatcag tctaatacatt aaaaaaaaaa aaaaaaaaaa 1227

<210> 36

<211> 1063

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (3)..(836)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 36

gc aaa gtg caa aaa ttt aaa gtt gga gac aaa gtt ggt gtt ggg tgc 47
 Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys
 1 5 10 15

ttg gta ggc tca tgc aaa act tgc gac agc tgt gct aac gat ttg gag 95
 Leu Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu
 20 25 30

aac tac tgc ccc aaa cag ata cag act tac ggc gcc aag tac ctt gac 143
 Asn Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp
 35 40 45

gga aca acc aca tac ggc ggt tac tct gac atc atg gtg gcg gat gag 191
 Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp Glu
 50 55 60

gcc ttt gta atc cgt att ccg gac aac ctg cct ctt gag ggt gct gct 239
 Ala Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala
 65 70 75

cct ctc cta tgt gcc gga atc aca act tac agt ccc ctg agg tat ttc 287
 Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe
 80 85 90 95

gga ctt gac aaa ccc ggc atg cat gtc ggg gtg gtt ggc ctt ggc ggt 335
 Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly
 100 105 110

tta ggc cat gtc gcg gtg aag ttt gcc aag gct ttg ggg gtt aat gtc 383
 Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val
 115 120 125

aca gtg atc agt acc tcc gct aat aag aaa gat gaa gct att aaa cac 431
 Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His
 130 135 140

ctt ggt gct gat tct ttc ttg gtc agt cgt gac caa gat cag atg cag	479
Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln	
145 150 155	
gct gcc atg gga aca ttg gac ggt atc atc gac aca gtt tcc gca gtc	527
Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val	
160 165 170 175	
cac ccc ctc cca cct ttg att agt tta ttg aag gct aat gga aag ctt	575
His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu	
180 185 190	
gtt atg gtt gga gca cca gag aag cca ctt gag cta cca gtt ttt tct	623
Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser	
195 200 205	
tta ata atg gga agg aag act tta gcc ggt agt aat atc gga ggt atc	671
Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile	
210 215 220	
aag gag aca caa gag atg ata gat ttg gca gcc aaa cac aac ata acg	719
Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr	
225 230 235	
gcc gac atc gag att atc ccc atc gac tat ttg aac act gct atg gag	767
Ala Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu	
240 245 250 255	
cgt ctt gct aaa ggg gat gtt aga tac cgt ttt gtc atc gac atc gga	815
Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly	
260 265 270	
aac aca ttg aag ccg gcc att taaatttgca tttcgatcag aaactgaatc	866
Asn Thr Leu Lys Pro Ala Ile	
275	
aagcgaggtc gagaggccta cgtaacaatg caaacatgtg ctagcttggt cttggagtag	926
tcttttagctt ttctctgatg tattccatct gttttgttca tgtcccatct tattatgaga	986
aaaatgtggg tacctgtggat attgaataaa tgaagagcta ctggaacgat ggtttcacaa	1046
aaaaaaaaa aaaaaaa	1063
<210> 37	
<211> 1228	
<212> DNA	
<213> Fragaria x ananassa	
<220>	
<221> CDS	
<222> (1)..(849)	
<223> partial cDNA	
<220>	
<223> Strawberry alcohol dehydrogenase	
<400> 37	
gca aga gat tca tct ggt gtc ctc tct ccc ttc aat ttc tcc aga agg	48
Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg	
1 5 10 15	

gaa acc gga gag aaa gac gtt atg ttc aaa gtg ttg tac tgt gga att Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile 20 25 30	96
tgc cat tcg gac ctt cac atg gtc aag aat gaa tgg ggc ttc tct acc Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr 35 40 45	144
tat cct ttg gtc ccg ggg cat gag att gtt ggt gaa gtt acg gaa gta Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val 50 55 60	192
ggg agc aaa gta caa aaa ttt aaa gtt gga gac aga gtc ggt gtt gga Gly Ser Lys Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly 65 70 75 80	240
tgc gtt gtg gga tct tgc cga tct tgt gaa aat tgt acc gac cac ctt Cys Val Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu 85 90 95	288
gag aac tac tgc ccc aaa cag ata ctc act tac ggt gcc aag tac tac Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr 100 105 110	336
gac gga acc acc acc tat ggc ggt tac tct gac att atg gtg gcc gac Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp 115 120 125	384
gaa cac ttc ata gta cgc atc cca gac aac ttg cct ctt gat ggc gct Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala 130 135 140	432
gcg ccg ctc cta tgt gcc ggg att aca acc tac agc ccc ctg aga tat Ala Pro Leu Leu Cys Glu Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr 145 150 155 160	480
ttc gga ctt gac aag ccc ggc atg cat gta ggt gtg gtc ggc cta ggc Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly 165 170 175	528
ggt tta ggc cac gtc gcc gtg aag ttt gcc aag gct atg gga gtg aag Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys 180 185 190	576
gtt aca gtg atc agt acg tcc cct aag aaa gag gag gaa gct ctt aaa Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Leu Lys 195 200 205	624
cac cta gga gct gac tcg ttt ttc gtt agc cgt gac caa gat caa atg His Leu Gly Ala Asp Ser Phe Phe Val Ser Arg Asp Gln Asp Gln Met 210 215 220	672
cag gct gcc att ggt acc atg gat ggg atc att gac aca gtt tct gca Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala 225 230 235 240	720
caa cat cct ctc ctg cct ttg att ggt ttg ttg aag tct cat gga aag Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys 245 250 255	768
ctt gtt atg gtt ggt gca cca gag aag cct ctt gaa ctt cca gtt ttt Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe	816

260 265 270

cct tta ctc atg gga aga aag atg ggt agc tgg taaccggcat ttgggggtat 869
 Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp
 275 280

gaaggagaca caagagatga tagattttgc tgccaggcac aacataacag cagacatcga 929
 agtcatacaa tcgactactt aaacactgct atggagcggt tagtcaaagc agatgtcaga 989
 taccgttttg tcatcgacat tggaacacaca ctgaaggcta gcacttaaata tctgcaatcc 1049
 agactgtatc aatgaagaaa caagaacaga aactgagatt gatttggtgt catactccgc 1109
 ctatggtttt ccttacagca ttttttgttg tttgctacat gaataacgat cacatgaact 1169
 gtgatgattt gataataaaaa gaatacataa acaaaaaaaaa caaaaaaaaa aaaaaaaaaa 1228

<210> 38
 <211> 852
 <212> DNA
 <213> Fragaria x ananassa

<220>
 <221> CDS
 <222> (3)..(566)
 <223> partial cDNA

<220>
 <223> Strawberry alcohol dehydrogenase

<400> 38

gt ccc ctg agg tat ttc gga ctt gac aaa ccc ggc atg cat gtc ggg 47
 Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly
 1 5 10 15

gtg gtt ggc ctt ggc ggt tta ggc cat gtc gcg gtg aag ttt gcc aag 95
 Val Val Gly Leu Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys
 20 25 30

gct ttg ggg gtt gag gtc aca gtg atc agt acc tcc gct aat aag aaa 143
 Ala Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys
 35 40 45

gat gaa gct att aaa cac ctt ggt gct gat tct ttc ttg gtc agt cgt 191
 Asp Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg
 50 55 60

gac caa gat cag atg cag gct gcc atg gga aca ttg gac ggt atc atc 239
 Asp Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile
 65 70 75

gac aca gtt tct gca gtc cac ccc ctc cca cct ttg att agt tta ttg 287
 Asp Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu
 80 85 90 95

aag gct aat gga aag ctt gtt atg gtt gga gca cca gag aag cca ctt 335
 Lys Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu
 100 105 110

gag cta cca gtt ttt tct tta ata atg gga agg aag act tta gcc ggt 383
 Glu Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly

115	120	125	
agt aat atc gga ggt atc aag gag aca caa gag atg ata gat ttg gca			431
Ser Asn Ile Gly Gly Ile Lys	Glu Thr Gln Glu Met	Ile Asp Leu Ala	
130	135	140	
gct aaa cac aac ata acg gcc gac atc gag gtc atc ccc atc gat tat			479
Ala Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr			
145	150	155	
ttg aac act gca atg gag cgt ctt gct aaa ggg gat gtt aga tac cgg			527
Leu Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg			
160	165	170	175
ttt gtc atc gac atc gga aac aca ttg aag ccg gcc act taaatttgca			576
Phe Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr			
180	185		
tttcgatcag aaactgaatc aagcgatgtc gagaggccta cgtaacaatg taaacatgtg			636
ctagcttggt cttgtagtag tcttttagcat ttctctgatg tactccttct gttttgttca			696
tgttccatct tataataaga ttcttattat gaaaaaata tgggtaccgtg gatattgaat			756
aatgaagaa ctactggaac aatgggtttca caaattatgtt gtggtgctaa aaaaaaaaaa			816
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa			852
<210> 39			
<211> 181			
<212> PRT			
<213> Fragaria x ananassa			
<223> Strawberry alcohol dehydrogenase			
<400> 39			
Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly			
1	5	10	15
Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His His			
20	25	30	
Ile Thr Val Ile Ser Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu Glu			
35	40	45	
His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln Met			
50	55	60	
Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro Val			
65	70	75	80
Phê His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly Lys			
85	90	95	
Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser Pro			
100	105	110	
Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly Glu			
115	120	125	
His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg Ala			
130	135	140	

Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala Phe
 145 150 155 160

Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp Cys
 165 170 175

Cys Arg Gln Gln Ser
 180

<210> 40

<211> 176

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 40

Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu
 1 5 10 15

Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala
 20 25 30

Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser
 35 40 45

Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly
 50 55 60

Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln
 65 70 75 80

Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg
 85 90 95

Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys
 100 105 110

Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro
 115 120 125

Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile
 130 135 140

Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe
 145 150 155 160

Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met
 165 170 175

<210> 41

<211> 283

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 41

Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly
 1 5 10 15

Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys
 20 25 30

Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu
 35 40 45
 Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His
 50 55 60
 Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe
 65 70 75 80
 Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly
 85 90 95
 Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr
 100 105 110
 Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys
 115 120 125
 Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala
 130 135 140
 Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly
 145 150 155 160
 Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu
 165 170 175
 Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln
 180 185 190
 Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile
 195 200 205
 Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys
 210 215 220
 Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr
 225 230 235 240
 Asp Leu Asn Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val
 245 250 255
 Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu
 260 265 270
 Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp
 275 280

<210> 42
 <211> 1010
 <212> DNA
 <213> Fragaria x ananassa

<220>
 <221> CDS
 <222> (2)..(850)
 <223> partial cDNA

<220>
 <223> Strawberry alcohol dehydrogenase

<400> 42

g gaa act acc atc aat ttt ggg tct aag aag att gca gtt gtt act gga 49
Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly
1 5 10 15

gcc aac aaa ggg att gga ctt gag att agc aag caa tta gct gct aaa 97
Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys
20 25 30

gga gtt ggg gtg gta tta aca gca aga gat gtg aag aga gga aca gaa 145
Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu
35 40 45

gct gct gaa aat ctt aag gct tct ggg ttc tct gat gtg gta ttt cat 193
Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His
50 55 60

cag cta gat gta aca gag ccg act act att ggt tct ttg gca aac ttt 241
Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe
65 70 75 80

ctt gaa acg caa ttt gga aag ctt gac ata ttg gtt aac aat gca gga 289
Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly
85 90 95

gtc gtt gga tct gta tac ctc aca gcc gac tat gat cca gtg caa aca 337
Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr
100 105 110

tac gag aca gcg agg gat tgt ttg aaa aca aac tat tat ggg ctc aag 385
Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys
115 120 125

caa gtc aca gaa gca ctt gtt ccg ctg ctt caa aaa tct gaa gct gca 433
Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala
130 135 140

agg ata gtc aat gtc tct tcc gga tta gga cag cta aga aat att gga 481
Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly
145 150 155 160

aat gag aag gcc aag aag gag cta gga gat gca gat aac ctc aac gag 529
Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu
165 170 175

gag aaa gtg gac aag cta gtt gag gaa ttt ctg gag gat gtg aaa cag 577
Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln
180 185 190

gat tcg ata gaa tcc aaa ggc tgg cct cta agt ata tct gcc tac att 625
Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile
195 200 205

gtc tca aaa gca gct ctg aat gct tat aca aga ctc ttg gca aag aag 673
Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys
210 215 220

tat ccc cat att gcc ata aac gca gtt ggt cca ggt tat acc aaa aca 721
Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr
225 230 235 240

gac ctc aat aat aat tcc ggg att ctc aca gtt gaa gaa gct gca gta 769
Asp Leu Asn Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val

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245                250                255
ggg cct gtg agg ctg gct ttg ata gcc gaa act aga att tcc ggc ctc 817
Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu
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ttc ttc aac aga aat gaa gag tcg acc ttt gat taggtcaacg tgatccctga 870
Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp
                275                280

tgaactggac tatttttagat tttcagaatg tgcttgattt tgttgaagta tttatgggat 930
ttgtatgtat actttgatgt atcattgtat taatagagca catgttgtga tcaaaaaaaaa 990
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<211> 243
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<213> Mangifera indica
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Phe Gly Ser Gly Gly Trp Gly Ser Ser Leu Ala Asp Thr Tyr Ser Arg
          20          25          30
Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp
          35          40          45
Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro
          50          55          60
Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu
          65          70          75          80
Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn
          85          90          95
Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met
          100          105          110
Leu Val Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu Gly Arg Lys
          115          120          125
Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu
          130          135          140
Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu
          145          150          155          160
Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr
          165          170          175
Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser
          180          185          190
Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu
          195          200          205

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Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser
 210 215 220

Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro
 225 230 235 240

Ala Glu Phe

<210> 44
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 <212> DNA
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<220>
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 <223> cDNA

<220>
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 1 5 10 15
 ttc gga tca ggt ggt tgg ggt tct tct ctt gct gac act tac tct cgc 96
 Phe Gly Ser Gly Trp Gly Ser Leu Ala Asp Thr Tyr Ser Arg
 20 25 30
 aag gct gat gta tta gtt cgt ggc tat ggt ggc tac aat act aga tgg 144
 Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Tyr Asn Thr Arg Trp
 35 40 45
 gca ttg ttc ttg tta tgt cac att ttc cct ctg cac aat aaa ata cct 192
 Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro
 50 55 60
 cca gcc gtc acc aca att ttc ttt ggg gct aat gat gca gcc ctt ctt 240
 Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu
 65 70 75 80
 ggg aga acg agt gaa agg cag cat gtt ccc gtg gaa gaa tac aag aac 288
 Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn
 85 90 95
 aat ctc aga aaa atg gtt cag cat ttg aag gaa gtc tcc ccc acg atg 336
 Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met
 100 105 110
 cta gtt gtg ctt att act cca cca cca att gat gag gaa ggg cgt aaa 384
 Leu Val Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu Gly Arg Lys
 115 120 125
 gca tat gca cga tcc gtt tat ggt gag aaa gct atg aaa gag cct gag 432
 Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu
 130 135 140
 agg aca aat gaa atg gct gga gtt tat gct aga cat tgt gtt gaa ctg 480
 Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu
 145 150 155 160

gca aaa gat ctt cct gcc att gat ctg tgg tcc aag atg cag gaa aca 528
 Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr
 165 170 175

gaa ggt tgg cag aaa aaa ttc ctc agt gat ggg ttg cac ctt aag tca 576
 Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser
 180 185 190

gaa ggc aat gca gtg gtt cac caa gaa gtt gtg aga gtt cta aaa gaa 624
 Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu
 195 200 205

gca tgg ttt tct cct gaa caa atg cca tat gat ttt cct cac caa tca 672
 Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser
 210 215 220

gta att gat gga aaa cac cct gag aaa gct ttc caa ctg caa tgc cct 720
 Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro
 225 230 235 240

gct gaa ttc tagtcaagac aggcttggaa atttggtctc tctttcaatt 769
 Ala Glu Phe

tttctatttg atgaaaagat ttggactgct ttttcctagt catgccaaat gaaacagtgt 829

tagccttttg cctatatttat cagatgctga tatgctctct gtgtcgac 877

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 <211> 12
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: various fruit

<220>
 <223> alcohol acyl transferase motif

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 1 5 10

<210> 46
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 <212> PRT
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<220>
 <223> alcohol acyl transferase motif

<220>
 <223> Xaa = any amino acid residue

<400> 46
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 1 5 10

<210> 47
 <211> 16

<212> PRT
 <213> Unknown Organism

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 <223> alcohol acyl transferase motif

 <220>
 <223> Xaa = any amino acid residue

 <400> 47
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 1 5 10 15

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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <220>
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <220>
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 <210> 50
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <223> PCR Primer

 <220>
 <223> AAP166

 <400> 50

cgtcgaccat tgcacgagcc acataatc

28